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Result
No.
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Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 s
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Maximum
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                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB seq length: 0
DB seq length: 2000000000
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Match
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997
1 EGDYSLCQQREKLDNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
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                                                                                                                                                                                                                                                                                                             Length
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               AAB19333
AAY23611
AAY236109
AAY23604
AAY23595
AAY23595
AAY23595
AAY23605
AAY23603
AAY23593
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A hookworm platele Neutrophil inhibit Canine hookworm ne Canine hookworm ne
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159	159	159	159	160	161.5	187	190	200	200	201	205	214	255	255	255.5	260	262	265.5	266	266	269	284.5	286.5	287	290	290	290	290	290	290	290	290	290	290
15.9	15.9	•	•	•		18.8	٠	0	•	•	•	21.5	٠	•	•	•		٠	٠				28.7										_	29.1
463	463	347	266	300	223	220	253	189	189	440	454	222	208	208	192	218	218	424	224	224	263	270	234	274	289	274	274	274	274	274	274	274	272	257
21	20	22										19	20	14	22	17	17	17	20	14	20	20	14	20	20	23	23	20	20	20	20	14	20	23
AAB01373	AAY13392	AAM41502	AAM39716	AAU08687	AAE13066	AAE13068	AAE13067	AAY23598	AAR52990	AAR26786	AAR26785	AAW37166	AAY23594	AAR52986	AAE13070	AAW04323	AAW04322	AAW04321	AAY23596	AAR52988	AAY23602	AAY23608	AAR52985	AAY23607	AAY23599	AAE20890	AAU97699	AAY23591	AAY23592	AAY23601	AAY23600	AAR42488	AAY23606	AAE20891
n-asso	-		pol vne	-		Onchocerca volvulu	וס		Š	3 (Sequence of a homo	מ		E				stoma sect	hookworm	hookworm	hookworm	hookworm	hookworm		Protein encoded by	NIFICE ins	Canine hookworm we	phil inhih	hookworm	hookworm	hookworm	hookworm	E	Ancylostoma canium

ALIGNMENTS

A hookworm platelet inhibitor polypeptide.

19-FEB-2001 (first entry)

AAB19333;

AAB19333 standard; Protein;

181

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RESULT 1
AAAB1933
ID AAB1
XX AAB1
AX AAB1
XX A
Novel platelet inhibitor from hookworms useful for veterinary and
                                                                                                          WPI; 2000-672551/65.
N-PSDB; AAA75998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hookworm platelet inhibitor; platelet aggregation; fibrinogen; collagen; platelet function; cancer; myocardial infarction; unstable angina; stroke; arterial angioplasty; thrombocytopenic purpura; malaria; haemolytic uremic syndrome; heparin-induced thrombosis; vaccine.
                                                                                                                                                                                                                                                 Cappello M, Chadderdon RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-1999; 99US-0127239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ancylostoma caninum.
                                                                                                                                                                                                                                                                                                                                                (UYYA ) UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAR-2000; 2000WO-US08519
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RESULT 2
AAX23611
ID AAX7
XX AAX
XX AX
DT 03
XX NE
EW 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local :
                                                                                                                                                                                                                                                                         Neutrophil inhibitory factor, NIF; mutant; shock; stroke; allograft rejection; vasculitis; autoimmune diabetes; ARDS; allograft rejection; vasculimatory skin disease; myocardial infarction; rheumatoid arthritis; inflammatory skin disease; myocardial infarction; inflammatory bowel disease; adult respiratory distress syndrome; ischemia-reperfusion injury; acute inflammation; bacterial infection; vaccine; parasitic worm infection; antihelminic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY23611;
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                                                                            26-MAY-1995;
                                                                                                                                                                                                                             Ancylostoma ceylanicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neutrophil inhibitory factor (AceNIF3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY23611 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 H 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  μ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 997; DB 21; llarity 100.0%; Pred. No. 2.1e-95; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36;
  93US-0173510
92US-0881721
                                                                            95US-0450497
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  RESULT 3
ANY 3609
ID ANY 27
AC ANY 2
AC ANY 2
XX 03-8
XX 03-8
XX W Neut
KW Allt
KW allt
KW 1161
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Best Local S
Matches 75
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11-MAY-1993;
10-NOV-1993;
26-MAY-1995;
Neutrophil inhibitory factor; NIF; mutant; shock; stroke; allograft rejection; vasculitis; autoimmune diabetes; ARDS; rheumatoid arthritis; inflammatory skin disease; myocardial infarction; inflammatory bowel disease; adult respiratory distress syndrome; ischemia-reperfusion injury; acute inflammation; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                      Canine hookworm neutrophil inhibitory factor AcaNIF9 polypeptide
                                                                                                                                                                                                     03-SEP-1999
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                                                                                                                                                                                                                                                       AAY23609;
                                                                                                                                                                                                                                                                                                       AAY23609 standard; Protein;
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DB; AAX85548.
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75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           920S-0996972.
930S-0060433.
930S-0151064.
950S-0450497.
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151

129

189

97 69

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The specification describes mutant Neutrophil Inhibitory Factors (NIFS), CC where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197, CC or 223 in the wild type sequence (see AnY23591) is replaced by a Gin Cresidue. NIFs may be useful for treating shock, stroke, acute and Cc chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid crespiratory distress syndrome (AnDs), ischemia reperfusion injury compounds of the faction, and acute inflammatory bowel disease, adult respiratory distress syndrome (AnDs), ischemia-reperfusion injury compounds of the faction, and acute inflammation caused by anterial infection such as sepsis or bacterial meningitis. NIFs or NIF compounds of the as vaccines against parasitic worm infection.

CC bacterial infection as vaccines against parasitic worm infection of anti-NIF antibodies may be useful for detecting infection of a mammalian compounds. Other NIF strom tissue homogenates, cloned cells etc. NIFs may be useful for the detection of NIF minics or antagonists in other compounds. Other NIF agonists and inhibitors may also be used as compounds. Other NIF agonists and inhibitors may also be used as compounds. Other NIF agonists and inhibitors may also be used as antihelminic agents. The present sequence represents a hookworm NIF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 22; Fig 9A-B; 131pp; English.
152 EEGAPCSRCSDYGAGVTCDDDWQNLLC 178
: | | | | | : : | | : : |
190 KVGVPCSNCTEYTRG-----DEEKVFC 211
                                                                                                                                                                                                                                                                                                                                                                                       70 DYDCDAEGSAYESAIKQCSSNKSSSAEYDENVYVIDNTYEDEVDPALKAISSWTSQAFNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 KGDEPTCKONNGSMTNELRRRFLRLHNGYRSILALGHVNISEESNETFLYAHRASRMRIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EGDYSLCOORE-KLDDDMREMFTELHNGYRA------AFARNYKTSKMRTM 44
                                                                                                                                                                                   VYDCTLEEKAYKSA-EKCSEEPSSE---EENVDVFSAA---TLNIPLEAGNSWWSEIFEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.4%; Score 323; DB 20; 36.2%; Pred. No. 3.5e-25; Live 31; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 238;
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infarction;

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The specification describes mutant Neutrophil Inhibitory Factors (NIFS), CC where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197, CC or 223 in the wild type sequence (see AnX23591) is replaced by a Gln CC chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid CC arthritis, inflammatory skin diseases, inflammatory bowel disease, adult CC respiratory distress syndrome (ARDS), ischemia-reperfusion injury CC chlowing myocardial infarction, and acute inflammation caused by bacterial infection such as sepsis or bacterial meningitis. NIFS or NIF CF fagments may be used as vaccines against parasitic worm infection of Anti-NIF antibodies may be useful for detecting infection of a mammalian CC compounds. Other NIF from tissue homogenates, caloned cells etc. NIFs may compounds. Other NIF agonists and inhibitors may also be used as compounds. Other NIF agonists and inhibitors may also be used as antihelminic agents. ANY23600-10 represent canine hookworm NIF proteins.
AAY23610 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-DEC-1993;
11-MAY-1992;
24-DEC-1992;
11-MAY-1993;
10-NOV-1993;
26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 21; Fig 16A-V; 131pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Foster DL, Moyle M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUL-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ancylostoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vaccine; parasitic worm infection; antihelminic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1999-403975/34.
DB; AAX85546.
                                                                                                                                                                                                                                   Similarity
79; Conser
                                                                                            KTIYEEGAPCSRCSDYGAGVTCDDD 172
                                                                                                                                                              EAFNLNKTGEGVVYRSILNISNFANLAWDTREKVGCAVVKCPSGNTHVVCHYPKIVKKEG
                                                                                                                                                                                  EIFEL----RGKVYNKNGKTSNIANMVWDSHDKLGCAVVDC-SGKTHVVCQYGPEAKGDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 AA;
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        canium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93US-0173510.
92US-0881721.
92US-0996972.
93US-0060433.
93US-0151064.
95US-0450497.
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  Protein;
                                                                                                                                                                                                                                                                                                                                                                                                          32.0%;
                                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                                                                                                                                      Score 319; DB 20;
Pred. No. 9.6e-25;
8; Mismatches 64;
₿
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 248;
                                                                                                                                                                                                                                                                                                                                                                                      Indels 44;
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                  147
                                                                                                                                                                                                                                       137
                                                                                                                                                                                                                                                                      92
                                                                                                                                                                                                                                                                                                              82
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                                                                                                                                                                                                                                                         The specification describes mutant Neutrophil Inhibitory Factors (NIFs), CC where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197, CC or 223 in the wild type sequence (see AAY23591) is replaced by a Glin CC chronic allograft rejection, vasculitis, sutchamune diabetes, rheumatoid, CC arthritis, inflammatory skin diseases, inflammatory bowel disease, adult CC respiratory distress syndrome (ARDS), ischemia reperfusion injury CC injury myocardial infarction, and acute inflammation caused by CC bacterial infection such as sepsis or bacterial anningitis. NIFS or NIF CC intimites may be used as vaccines against parasitic worm infection. CC in the control of the same of the detection of the same of the detection of the same of the detection of the same of the compounds. Other NIF agonists and inhibitors may also be used as compounds. Other NIF agonists and inhibitors may also be used as compounds. Other NIF agonists and inhibitors may also be used as compounds. Other NIF agonists and inhibitors may also be used as compounds.
                                                                                                                                                          Query Match
Best Local S
Matches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-DEC-1993;
11-MAY-1992;
24-DEC-1992;
11-MAY-1993;
10-NOV-1993;
26-MAY-1995;
                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neutrophil inhibitory factor; NIF; mutant; shock; stroke; allograft rejection; vasculitis; autoimmune diabetes; ARDS; rheumatoid arthritis; inflammatory skin disease; myocardial infarctio; inflammatory bowel disease; adult respiratory distress syndrome; ischemia-reperfusion injury; acute inflammation; bacterial infection; vaccine; parasitic worm infection; antihelminic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 21; Fig 16A-V; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammatory responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mutant Neutrophil Inhibitory Factors useful for treating inflammatory conditions and especially to prevent or dec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-403975/34.
N-PSDB; AAX85547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Foster DL, Moyle M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canine hookworm neutrophil inhibitory factor AcaNIF18 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CORV-) CORVAS INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ancylostoma canium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY23610;
           71
                                            38
                                                                                 1
                                                                                                                       -
                                                                                                                                                          80; Conserv
                        TSKMRTMVYDCTLEEKAYKSAEKCSEEPSSEE---ENV------DVFSAATLNIPLEAG
                                                                                                       EGDYSLCQQREKL----DDDMREMFTELHNGYRAAFARNY-----K
    ASKMRYLKYDCEAEKSAYESAKKCQTTAFSWEKYDENLQVIEDPRDINHAA----
                                                                             EHDPTCPQNGEKMEKGFDDAMRLKFLALHNGYRSRLALGHVSITEESEDYDLYDLLYAPT
                                                                                                                                                                                                                                241 AA;
                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93US-0173510.
92US-0881721.
92US-0996972.
93US-0060433.
93US-0151064.
95US-0450497.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-0450497
                                                                                                                                                                         30.7%;
                                                                                                                                                     Score 306.5; DB 20; Pred. No. 1.8e-23; 19; Mismatches 68;
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RESULT 4
AAY23610
ID AAY2

밁 δÃ 밁 Š 문 Ş

93

Query Match Best Local S Matches 79

23

Sequence

₽ Š

198

148 138

> Indels 43; Length 241;

Gaps

-LKAI 125

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ARESULT 5
ANATAMAN
AN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                    The specification describes mutant Neutrophil Inhibitory Factors (NIFs), where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197, CC or 223 in the wild type sequence (see ANZ3359) is replaced by a Gin CC residue. NIFs may be useful for treating shock, stroke, acute and cc chronic allogatef rejection, vasculitis, autoimmune diabetes, rheumatoid CC arthritis, inflammatory skin diseases, inflammatory bowel disease, adult crespiratory distress syntome (ARDS), ischemia-reperfusion injury CC following myocardial infarction, and acute inflammation caused by NIF CC fragments may be used as vaccines against parasitic worm infaction. CC Anti-NIF antibodies may be useful for detecting infaction of a mammalian CC and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may CC compounds. Other NIF agonists and inhibitors may also be used as compounds. Other NIF agonists and inhibitors may also be used as CC anti-NIF and detection of NIF minics or antagonists in other CC compounds. Other NIF agonists and inhibitors may also be used as CC anti-Nie agonists. AAY23600-10 represent canine hookworm NIF proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-DEC-1993;
11-MAY-1992;
24-DEC-1992;
11-MAY-1993;
10-NOV-1993;
26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neutrophil inhibitory factor, NIF, mutant; shock; stock; stock; allograft rejection; vasculitis; autoimmune diabetes; ARDS; rheumatoid arthritis; inflammatory skin disease; myocardial infarction; inflammatory bowel disease; adult respiratory distress syndrome; ischemia-reperfusion injury; acute inflammation; bacterial infection; vaccine; parasitic worm infection; antihelminic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Canine hookworm neutrophil inhibitory factor AcaNIF4 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mutant Neutrophil Inhibitory Factors useful for treating inflammatory conditions and especially to prevent or decrease inflammatory responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-JUL-1999
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    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 21; Fig 16A-V; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Foster DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CORV-) CORVAS INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ancylostoma canium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY23604 standard; Protein; 274 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1999-403975/34.
DB; AAX85541.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VEKEGKPIYTTGVPCRGCSGYANKFFCHAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKGDGKTIYEEGAPCSRCSDYGAGVTCDDD 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISWATEAFNLNKTGEGVVYRSILNISNFANLAWDTREKVGCAVVKCSPRTTHVVCHYPKI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NSWWSEIFEL----RKVYNKNGKTSNIANMYWDSHDKLGCAVVDCSGK-THVVCQYGPE 142
    274 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Moyle M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93US-0173510.
92US-0881721.
92US-096972.
92US-0060433.
93US-0151064.
95US-0450497.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 32.6
Conservative
                                                                                                                                                                                                                                                                                                                                                                               23-DEC-1993;
11-MAY-1992;
24-DEC-1992;
11-MAY-1993;
The specification describes mutant Neutrophil Inhibitory Factors (NIFs), where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197, or 223 in the wild type sequence (see AAV23591) is replaced by a Gln residue. NIFs may be useful for treating shock, stroke, acute and chronic allograft rejection, vasculitis, autoimune diabetes, rheumatoid arthritis, inflammatory skin diseases, inflammatory bowel disease, adult respiratory distress syndrome (ARDS), ischemia-reperfusion injury following myocardial infarction, and acute inflammation caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neutrophil inhibitory factor; NIF; mutant; shock; stroke; allograft rejection; vasculitis; autoimmune diabetes; ARDS; rheumatoid arthritis; inflammatory skin disease; myocardial infarction; inflammatory bowel disease; adult respiratory distress syndrome; ischemia-reperfusion injury; acute inflammation; bacterial infection; vaccine; parasitic worm infection; antihelminic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Canine hookworm neutrophil inhibitory factor isoform clone 3FL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY23595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY23595 standard; Protein;
                                                                                                                                                  Example 10; Fig 9A-E; 131pp; English.
                                                                                                                                                                                 Mutant Neutrophil Inhibitory Factors useful for treating inflammatory conditions and especially to prevent or decrease inflammatory responses
                                                                                                                                                                                                                                                 WPI; 1999-403975/34.
                                                                                                                                                                                                                                                                                Foster DL,
                                                                                                                                                                                                                                                                                                                                                26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                 10-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ancylostoma caninum.
                                                                                                                                                                                                                                                                                                                 (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 T-----HVVCQYGPEAKGDGKTIYEEGAPCSRCSDYGAGV-----TCDDD 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 -KTSKMRTMYYDCTLEEKAYKSAEKC---SEEPSSEEENVDVFSAATLNI---PLEAGNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 MCERNETEMPGFNDSMRLQFLAMHNGYRSLLALGHVGISKQPIDDDYYDDDYYYFYSSYA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 LCQQREK----LDDDMREMFTELHNGYRAAFARNY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYATAIHVVCHYPKILEKEEKQIYEVGKPCDRCSEYSKNANNITSPNWVCNDD 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WAKEAFNLNKTEEGEGYLYRSNHDISNFANLAWDTREKFGCAVVNCPLGEIDTTSNRDGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WWSEIFEL-----RGKYYNKNGKTSNIANMYWDSHDKLGCAVVDC------SGK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRASKMRYLEYDCEAEKSAYVSASNCSNISSPPEGYDENKYIFENSN-NISEAALKAMIS 138
                                                                                                                                                                                                                                                                                Moyle M;
                                                                                                                                                                                                                                                                                                                                                                               93US-0173510.
92US-0881721.
92US-0996972.
93US-0060433.
                                                                                                                                                                                                                                                                                                                                                  950S-0450497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.5%; Score 304.5; 32.6%; Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               231 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .5e-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9;
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RESULT 7
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ID AAAS
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AC AAAS
AC AAAS
AC CAAIS
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Best Local S
Matches 74
A canine hookworm cDNA library was screened with a probe amplified using primers 30.2 and 43.3.RC(AAQ52476 and AAQ52477, respectively) which ware based on sequences of isolated NIF peptide fragments. Se of the 120 positive clones were isolated for sequence analysis. One
                                                                                                                                                  Example
                                                                                                                                                                                                 New neutrophil inhibitory factor from parasitic worms - for preventing and treating inflammation, also derived nucleic vectors, transformed hosts and antibodies
                                                                                                                                                                                                                                                                                                             WPI; 1993-386208/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-MAY-1992;
24-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neutrophil inhibitory nematode; parasitic wo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Canine hookworm Neutrophil Inhibitory Factor isoform 2FL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-NOV-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9323063-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ancylostoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR52987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR52987 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                      (CORV-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                                      CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KTSKMRTMVYDCTLEEKAYKSAEKCSEEPSSE-----EENVDVFSAATLNIPLEA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHY-PKIEGEEKEGKQIYKVGTPCGDCSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CQYGPEAKG---DGKTIYEEGAPCSRCSDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SASKMRYMEYDCEAEKSAYKSASSCSDSSSSPEGYDENKYILENSSNISEAARLAI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -LSWAKEAFDLNKTGEGVLYRSNLTISNFANLAWDTREKFGCAVAKCPLKDTSATTIHVV
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                                                                                                                                              Fig
                                                                                                                                                                                                                                                                                                                                                             Moyle M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         920S-0881721.
920S-0996972.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       worm;
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                                                                                                                                                                                                                                                                                                                                                                   Vlasuk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tor; NIF; glycoprotein; endoparasite;
canine hookworm; peritoneal inflammation.
                                                                                                                                           English.
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                                                                                                                                                                                                                                                                                                                                                                GP;
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Pred. No. le-22;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 75
                                                                                                                                                                                                                                                                                                        23-DEC-1993;
11-MAY-1992;
24-DEC-1992;
11-MAY-1993;
10-NOV-1993;
26-MAY-1995;
                                            Mutant Neutrophil Inhibitory inflammatory conditions and inflammatory responses
                                                                                                                                             WPI; 1999-403975/34.
N-PSDB; AAX85542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US5919900-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neutrophil inhibitory factor; NIF; mutant; shock; stroke; allograft rejection; vasculitis; autoimmune diabetes; ARDS; rheumatoid arthritis; inflammatory skin disease; myocardial inflammatory bowel disease; adult respiratory distress syndrischemia-reperfusion injury; acute inflammation; bacterial i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        isolate, designated clone IFL, encoded an 825 nucleotide open reading frame (AAQ52475). The other clones contained partial ORFs and encoded partial NEP polypeptides (see AAR52995-R52990) which are thought to represent six NIF isoforms that are significantly similar to, but not identical to, the prototypical NIF-IFL polypeptide (AAR42488).
                                                                                                                                                                                                                                                           (CORV-) CORVAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ancylostoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccine; parasitic worm infection; antihelminic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canine hookworm neutrophil inhibitory factor AcaNIF6 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHY-PKIEGEEKEGKQIYKVGTPCGDCSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GNSWWSEIFEL----RGKVYNKNGKTSNIANMVWDSHDKLGCAVVDC-----SGKT-HVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KTSKMRTMYYDCTLEEKAYKSAEKCSEEPSSE------EENVDVFSAATLNIPLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CQYGPEAKG---DGKTIYEEGAPCSRCSDY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -LSWAKEAFDLNKTGEGVLYRSNLTISNFANLAWDTREKFGCAVAKCPLEDTSATTIHVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SASKMRYMEYDCEAEKSAYKSASSCSDSSSSPEGYDENKYILENSSNISEAARLAI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ICSQNGTGMFGFNDSMRLKFLEMHNGYRSRLALGHISITEEPESYDDDDDYGYSEVLYAP
                                                                                                                                                                                                               Moyle M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     canium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                     93US-0173510.
92US-0881721.
92US-0996972.
93US-0060433.
93US-0151064.
95US-0450497.
                                                                                                                                                                                                                                                           INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9505-0450497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
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                                                                  / Factors useful especially to pa
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Pred. No. 1.3e-22;
); Mismatches 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₿
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                                                                     prevent
                                                                  for treating revent or dec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Example 21;

Fig 16A-V; 131pp; English

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RESULT 9
AAY:
AC AAY:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 72
                      23-DEC-1993;
11-MAY-1992;
24-DEC-1992;
11-MAY-1993;
10-NOV-1993;
26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                               Neutrophil inhibitory factor; NIF; mutant; shock; stroke; allograft rejection; vasculitis; autoimmune diabetes; ARDS; rheumatoid arthritis; inflammatory skin disease; myocardial infarctio; inflammatory bowel disease; adult respiratory distress syndrome; ischemia-reperfusion injury; acute inflammation; bacterial infection; vaccine; parasitic worm infection; antihelminic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Canine
                                                                                                                                                                                                                    26-MAY-1995;
                                                                                                                                                                                                                                                                        06-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hookworm neutrophil inhibitory factor AcaNIF3 polypeptide
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72; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EAFNLNKTEKGVLYQPNHDISNFANLAWDTREKFGCAVVNCPLGEIDADIYDEETYATTI 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EIFEL----RGKYYNKNGKTSNIANMVWDSHDKLGCAVVDC------SGKT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKMRTMVYDCTLEEKAYKSAEKCSEE---PSSEEENVDVFSAATLNI---PLEAGNSWWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKMRYLEYDCEAERSAYTSASDCSDSSSPPEGYDENKYIFENSN-NISEAALKAMISWAK 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MCQQNETEMPGFNDLMRLQFLAMHNGYRSKLALGHISITDESESDYDYDYGFLPDFAPSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.7%;
milarity 34.3%;
Conservative 2
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                                                                                                                                                                                                                                                                                                                                                                                     canium.
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                      93US-0173510.
92US-0881721.
92US-0996972.
93US-0060433.
93US-0151064.
95US-0450497.
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Pred. No. 2.3e
22; Mismatches
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les 63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infarction;
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The Anti-NIF antibodies may be useful for detecting infection of a mammalian and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may be useful for the detection of NIF minics or antagonists in other compounds. Other NIF agonists and inhibitors may also be used as antihelminic agents. AAY23600-10 represent canine hookworm NIF proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 72
                                                         Neutrophil inhibitory factor: NIF; mutant; shock; stroke; allograft rejection; vasculitis; autoimmune diabetes; ARDS; rheumatoid arthritis; inflammatory skin disease; myocardial infarction; inflammatory bowel disease; adult respiratory distress syndrome; ischemia-reperfusion injury; acute inflammation; bacterial infection; vaccine; parasitic worm infection; antihelminic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mutant Neutrophil Inhibitory inflammatory conditions and einflammatory responses
                                                                                                                                                                    Canine hookworm neutrophil inhibitory factor isoform clone
                                                                                                                                                                                                   03-SEP-1999
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                              Ancylostoma
                                                                                                                                                                                                                                AAY23593;
                                                                                                                                                                                                                                                             AAY23593 standard;
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DB; AAX85540.
                                                                                                                                                                                                                                                                                                                                       201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 LCQQREK----LDDDMREMFTELHNGYRAAFARNY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MCQQNETEMPGFNDLMRLQFLAMHNGYRSKLALGHISITDESESDYDYDYGFLPDFAPSA
                                                                                                                                                                                                                                                                                                                                                                                                 SKMRYLEYDCEAERSAYTSASDCSDSSSPPEGYDENKYIFENSN-NISEAALKAMISWAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKMRTMYYDCTLEEKAYKSAEKCSEE---PSSEEENVDVFSAATLNI---PLEAGNSWWS
                                                                                                                                                                                                                                                                                                                                                                   HVVCQYGPEAKGDGKTIYEEGAPCSRCSDY 163
                                                                                                                                                                                                                                                                                                                                       HVVCHYPKINKTEGEPIYKVGTPCDDCSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                270 AA;
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                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                               Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 296.5;
Pred. No. 2.3e
22; Mismatches
                                                                                                                                                                                                                                                               232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ? Factors useful for treating
especially to prevent or dec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53;
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RESULT 1
AAE20891
ID AAE
XX
AC AAE
AC AAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
               01-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-DEC-1993;
11-MAY-1992;
24-DEC-1992;
11-MAY-1993;
10-NOV-1993;
26-MAY-1995;
                                                 AAE20891;
                                                                                AAE20891 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 10; Fig 9A-E; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mutant Neutrophil Inhibitory Factors useful for treating inflammatory conditions and especially to prevent or decrease inflammatory responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-403975/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUL-1999
                                                                                                                                                                  212
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                                                                                                                                                                                                                                                                                                                                                                                                                      1 Similarity 37.
                                                                                                                                                              SRRKENPIYTTGNRCGGCSDY 232
                                                                                                                                                                                 AKGDGKTIYEEGAPCSRCSDY 163
                                                                                                                                                                                                                     ISWATEAFNLNKTGEGVVYRSILDISNFANLAWDTREKVGCAVVKCSPRTTHVVCHYPKK 211
                                                                                                                                                                                                                                                  NSWWSEIFEL----RGKVYNKNGKTSNIANNVWDSHDKLGCAVVDCSGK-THVVCQYGPE 142
                                                                                                                                                                                                                                                                                    ASKMRYLKYDCEAEKSAYESAKKCQTTASSWEKYDENLQVIEDPKDINHAA-----LKAI
                                                                                                                                                                                                                                                                                                               TSKMRTMYYDCTLEEKAYKSAEKCSEEPSSEE---ENV------DVFSAATLNIPLEAG
                                                                                                                                                                                                                                                                                                                                                 EHDPTCPQNGEKMEKGFDDAIRLKFLAMHNGYRSRLALGHVSITEESEDYDLYDLLYAPR
                                                                                                                                                                                                                                                                                                                                                                          EGDYSLCOQREKL----DDDMREMFTELHNGYRAAFARNY------K 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           232 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93US-0173510.
92US-0881721.
92US-0996972.
93US-0060433.
93US-0151064.
95US-0450497.
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                                                                                                                                                                                                                                                                                                                                                                                                                          23;
                                                                                257
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 290.5; DB 20;
Pred. No. 8e-22;
3; Mismatches 60;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
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CC inhibitory factor (NIF) comprising growing a cell line expressing NIF CC inhibitory factor (NIF) comprising growing a cell line expressing NIF CC in an animal component free medium selected from inoculum growth medium. CC culture. The method is useful for preparation of NIF. Animal component CC free production growth medium is useful for preparation of NIF. Animal component CC production growth medium is useful for preparation of recombinant CC production. NIF is useful for preventing or treating inflammatory conditions characterised by abnormal neutrophil activation, for treating CC antoimmune diabetes, rheumatoid arthritis, head trauma, inflammatory beach of a securities of the cauchy inflammatory bowel disease, adult respiratory distress CC syndrome (ARDS), ischaemia-reperfusion injury following myocardial infarction, in which neutrophil infiltration and activation has been complicated and acute inflammation caused by bacterial infection, such as sepsis or bacterial meningitis. NIF is also useful as diagnostic agents, CC antagonists for their ability to affect NIF minics or to detect NIF creepfur, as a vaccine against parasitic worm infections. The present sequence is Ancylostoma canium mature NIF1 protein.
                                                                                                                                                                                                            Query Match
Best Local S
Matches 69
                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Preparing Neutrophil Inhibitory Factor for treating shock, by cell line expressing the factor in animal component-free medi inoculum growth medium, production growth medium or nutrient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 42; Page 92-94; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PFIZ )
(CORV-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neutrophil inhibitory factor; NIF; therapy; inflammatory condition; abnormal neutrophil activation; shock; stroke; allograft rejection; vasculitis; autoimmune diabetes; rheumatoid arthritis; head trauma; inflammatory skin disease; inflammatory bowel disease; antibacterial; adult respiratory distress syndrome; ARDS; ischaemla-reperfusion injury; myocardial infarction; bacterial infection; sepsis; cerebroprotective; bacterial meningitis; immunosuppressive; antiparasitic; antihelminthic; vascune; antilnflammatory; vasotropic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-292063/33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-AUG-2000; 2000US-0644942
28-FEB-2001; 2001US-0797410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-AUG-2001; 2001WO-US25733.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ancylostoma canium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ancylostoma canium mature neutrophil inhibitory factor (NIF) 1 protein.
99 GKYYNKNGKTSNIANMYWDSHDKLGCAYVDC:
                                                            78
                                                                                                 13
                                                                                                                                   18
                                                                                                                                                                        14
                                                                                                                                                                                                            69;
                                                                                                                                                                                                          29.1%;
Similarity 34.3%;
59; Conservative :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFIZER PROD INC.
CORVAS INT INC.
                                                                                                                                                    EKSAYMSARNCSDSSSPPEGYDENKYIFENSN-NISEAALKAMISWAKEAFNLNKTKEGE 136
                                                                             EEKAYKSAEKCSEE---PSSEEENVDVFSAATLNI---PLEAGNSWWSEIPEL-----R
                                                                                                                               NDSTRIQFLAMHNGYRSKLALGHISITEESESDDDDDFGFLPDFAPRASKMRYLEYDCEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ll SB, Geldart RW,
Hawrylik SJ, Moyl
                                                                                                                                                                                                                                                                                  257 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Moyle
                                                                                                                                                                                                          23;
                                                                                                                                                                                                        Score 290; DB 23;
Pred. No. 1e-21;
3; Mismatches 57,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ¥ 6
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                                                                                                                                                                                                        57;
                                                                                                                                                                                                                                           Length 257;
                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     k, by growing medium such a rient feed -
                                                                                                                                                                                                        52;
                                                                                                                                                                                                    Gaps
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밁 Š ₽

197 143 137

03-SEP-1999

AAY23606 standard;

98

50

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The specification describes mutant Neutrophil Inhibitory Factors (NIFs), 20 where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197, 20 or 223 in the wild type sequence (see AAV23591) is replaced by a Gin cesidue. NIFs may be useful for treating shock, stroke, acute and chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid arthritis, inflammatory skin diseases, inflammatory bowel disease, adult respiratory distress syndrome (ARDS), ischemia-reperfusion injury following myocardial infarction, and acute inflammation caused by bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF fragments may be used as vaccines against parasitic worm infection. Anti-NIF antibodies may be useful for detecting infection of a mammalian thost by a parasitic worm, as antihelminic agents, and in the detection can disolation of NIF from tissue homogenates, cloned cells etc. NIFs may be useful for the detection of NIF mimics or antagonists in other compounds. Other NIF agonists and inhibitors may also be used as compounds. Other NIF agonists and inhibitors may also be used as compounds. Other NIF agonists and inhibitors may also be used as compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mutant Neutrophil Inhibitory Factors useful for treating inflammatory conditions and especially to prevent or decrease inflammatory responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neutrophil inhibitory factor; NIF; mutant; shock; stroke; allograft rejection; vasculitis; autoimmune diabetes; ARDS; rheumatoid arthritis; inflammatory skin disease; myocardial infarction inflammatory bowel disease; adult respiratory distress syndrome; ischemia-reperfusion injury; acute inflammation; bacterial infection; vaccine; parasitic worm infection; antihelminic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Canine hookworm neutrophil inhibitory factor AcaNIF7 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 21; Fig 16A-V; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CORV-) CORVAS INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AKGDGKTIYEEGAPCSRCSDY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NKTEGOPIYKVGTPCDDCSEY 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GYLYRSNHDISNFANLAWDAREKFGCAVVNCPLGEIDDETNHDGETYATTIHVVCHYPKI 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93US-0173510.
92US-0881721.
92US-0996972.
93US-0060433.
93US-0151064.
95US-0450497.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         272
     Score
Pred.
     290; DB 20;
No. 1.1e-21;
                      Length
                         272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infarction;
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AAR42488
ID AAR42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
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                                             Matches
                                                                 Query Match
Best Local
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                                                                                                                                                                A canine hookworm cDNA library was screened with a probe amplified using primers 30.2 and 43.3 (AAQ52476 and AAQ52477, respectively) which were based on sequences of isolated NIF peptide fragments. Seven of the 120 positive clones were isolated for sequence analysis. One isolated designated clone IFL, encoded an 825 nucleotide open reading frame (AAQ52475). The other clones contained partial ORFs and encoded partial NIF polypeptides (see AAR5285-R52990) which are thought to represent six NIF isoforms that are significantly similar to, but not identical to, the prototypical NIF-IFL polypeptide (AAR42488).
                                                                                                                                                                                                                                                                                                                                                                                                                          New neutrophil inhibitory factor from parasitic worms - for preventing and treating inflammation, also derived nucleic vectors, transformed hosts and antibodies
                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                    Claim 23; Fig 8; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1993-386208/48.
N-PSDB; AAQ52475.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-MAY-1992;
24-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neutrophil inhibitory factor; NIF; glycoprotein; endoparasite;
nematode; parasitic worm; canine hookworm; peritoneal inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canine hookworm Neutrophil Inhibitory Factor 1FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR42488 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Foster DL, Moyle M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORV-) CORVAS INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9323063-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ancylostoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR42488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 NKTEGQPIYKVGTPCDDCSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 AKGDGKTIYEEGAPCSRCSDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93
       14 DDDMREMFTELHNGYRAAFARNY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99 GKVYNKNGKTSNIANMVWDSHDKLGCAVVDC------SGKT-----HVVCQYGPE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 DDDMREMFTELHNGYRAAFARNY------KTSKMRTMVYDCTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 EEKAYKSAEKCSEE---PSSEEENVDVFSAATLNI---PLEAGNSWWSEIFEL-----R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 NDSIRLQFLAMHNGYRSKLALGHISITEESESDDDDDDFGFLPDFAPRASKMRYLEYDCEA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69;
                                             69;
                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVLYRSNHDISNFANLAWDAREKFGCAVVNCPLGEIDDETIHDGETYATTIHVVCHYPKI 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKSAYMSARNCSDSSSPPEGYDENKYIFENSN-NISEAALKAMISWAKEAFNLNKTEEGE 151
                                                                                                                               274 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92US-0881721.
92US-0996972.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93WO-US04502
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                                             23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23;
                                          Score 290; DB
Pred. No. 1.1e
23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               274 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                             DB 14;
..le-21;
hes 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57;
                                                                                     Length 274;
                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
     --- KTSKMRTMVYDCTL 50
                                               52;
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                                             Gaps
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ARESULT 12

ARX23606

ID 23608

ID 23608

ID 23608

AX X XX

AX AX23

AX AX23

AX CAN13

AX CAN13

AX CAN14

AX CAN15

AX CAN11

AX CAN1

WPI; 1999-403975/34. N-PSDB; AAX85543.

Foster DL,

Moyle M;

23-DEC-1993; 11-MAY-1992; 24-DEC-1992; 11-MAY-1993; 10-NOV-1993; 26-MAY-1995;

26-MAY-1995; 06-JUL-1999 US5919900-A. Ancylostoma canium.

Query Match Best Local Similarity

Sequence

272 AA;

멓 Š

143 214

154

99 95

03-SEP-1999 AAY23600; 84 PP PP PP

35 51

may

98

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Neutrophil inhibitory factor; NIF; mutant; shock; stroke; allograft rejection; vasculitis; autoimmune diabetes; ARDS; rheumatoid arthritis; inflammatory skin disease; myocardial infarction; inflammatory bowel disease; edult respiratory distrass syndrome; ischemia-reperfusion injury; acute inflammation; bacterial infection; vaccine; parasitic worm infection; antihalminic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Canine hookworm neutrophil inhibitory factor NIF-1FL polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY23600 standard; Protein;
The specification describes mutant Neutrophil Inhibitory Factors (NIFS), where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197, or 223 in the wild type sequence (see ANY2591) is replaced by a Gibronic allograft rejection, vasculitis, autoimune diabetes, rheumatoid arthritis, inflammatory skin diseases, inflammatory bowel disease, adult respiratory distress syndrome (ARDS), ischemia-reperfusion the subjection of tragments may be used as vaccines against parasitic worm infection and the subjection of a mammalian anti-NIF antibodies may be useful for detecting infection of a mammalian host by a parasitic worm, as antihelminic agents, and in the detection of
                                                                                                                                                                                                                                                                        Mutant Neutrophil Inhibitory Factors useful for treating inflammatory conditions and especially to prevent or decrease inflammatory responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ancylostoma canium.
                                                                                                                                                                                                                                                                                                                                               WPI; 1999-403975/34.
N-PSDB; AAX85537.
                                                                                                                                                                                                                                       Example 21; Fig 16A-V; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GKYYNKNGKTSNIANMYWDSHDKLGCAVVDC------SGKT-----HVVCQYGPE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EEKAYKSAEKCSEE---PSSEEENVDVFSAATLNI---PLEAGNSWWSEIFEL-----R 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NKTEGOPIYKVGTPCDDCSEY 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AKGDGKTIYEEGAPCSRCSDY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GYLYRSNHDISNFANLAWDAREKFGCAVVNCPLGEIDDETNHDGETYATTIHVVCHYPKI 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKSAYMSARNCSDSSSPPEGYDENKYIFENSN-NISEAALKAMISWAKEAFNLNKTKEGE 153
                                                                                                                                                                                                                                                                                                                                                                                                  Moyle M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93US-0173510.
92US-0881721.
92US-0996972.
93US-0060433.
93US-0151064.
95US-0450497.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and isolation of NIF from tissue homogenates, cloned cells etc. NIFs man be useful for the detection of NIF minics or antisponists in other compounds. Other NIF agonists and inhibitors may also be used as antihelminic agents. AAY23600-10 represent canine hookworm NIF proteins
                                                                                                                                                                                                                                                             23-DEC-1993;
11-MAY-1992;
24-DEC-1992;
11-MAY-1993;
10-NOV-1993;
26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neutrophil inhibitory factor: NIF; mutant; shock; stroke; allograft rejection; vasculitis; autoimmune diabetes; ARDS; allograft arbititis; inflammatory skin disease; myocardial infarction; rheumatoid arthititis; inflammatory skin disease; myocardial infarction; inflammatory bowel disease; adult respiratory distress syndrome; inflammation; bacterial infection; ischemia-reperfusion injury; acute inflammation; bacterial infection; vaccine; parasitic worm infection; antihelminic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canine hookworm neutrophil inhibitory factor PCR-NIF7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY23601 standard; Protein;
                                                             Mutant Neutrophil Inhibitory Factors useful for treating inflammatory conditions and especially to prevent or decinflammatory responses
                                                                                                                                                                                                                                                                                                                                                                                           26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                US5919900-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ancylostoma canium.
                                                                                                                                                                                       Foster DL, Moyle M;
                                                                                                                                                                                                                        (CORV-) CORVAS
                                 Example
                                                                                                                                    WPI; 1999-403975/34.
N-PSDB; AAX85538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 DDDMREMFTELHNGYRAAFARNY-----------KTSKMRTMVYDCTL 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 Similarity 34.: 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NKTEGQPIYKVGTPCDDCSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKSAYMSARNCSDSSSPPEGYDENKYIFENSN-NISEAALKAMISWAKEAFNLNKTKEGE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEKAYKSAEKCSEE---PSSEEENVDVFSAATLNI---PLEAGNSWWSEIFEL-----R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NDSTRLOFLAMHNGYRSKLALGHISITEESESDDDDDFGFLPDFAPRASKMRYLEYDCEA 94
                                 21; Fig 16A-V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AKGDGKTIYEEGAPCSRCSDY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      274 AA;
                                                                                                                                                                                                                                                                93US-0173510.
92US-0881721.
92US-0996972.
93US-0060433.
93US-0151064.
95US-0450497.
                                                                                                                                                                                                                            INT INC
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                                 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 290; DB 20;
; Pred. No. 1.1e-21;
23; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234
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                                                                                          or decrease
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polypeptide.

Foster

DL,

23-DEC-1993; 11-MAY-1992; 24-DEC-1992; 11-MAY-1993; 10-NOV-1993; 26-MAY-1995;

US5919900-A.

06-JUL-1999.

26-MAY-1995;

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CC The specification describes mutant Neutrophil Inhibitory Factors (NIFs), cc where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197, cc or 223 in the wild type sequence (see ANY23551) is replaced by a Gln cc residue. NIFs may be useful for treating shock, stroke, acute and cc chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid cc arthritis, inflammatory skin diseases, inflammatory bowel disease, adult crespiratory distress syndrome (ANDS), ischemia-reperfusion injury cc following myocardial infarction, and acute inflammation caused by anterial infection such as sepsis or bacterial meningitis. NIFs or NIF cc fragments may be used as vaccines against parasitic worm infection. Cc hati-NIF antibodies may be useful for detecting infection of a mammalian cc host by a parasitic worm, as antihalminic agents, and in the detection and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may cc compounds. Other NIF agonists and inhibitors may also be used as cc antihalminic agents. ANY23600-10 represent canine hookworm NIF proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                         23-DEC-1993;
11-MAY-1992;
24-DEC-1992;
11-MAY-1993;
                                                                                                                                                                                                                                                                                                                      Neutrophil inhibitory factor, NIF; mutant; shock; stroke; allograft rejection; vasculitis; autoimmune diabetes; ARDS; rheumatoid arthritis; inflammatory skin disease; myocardial infarction; inflammatory bowel disease; adult respiratory distress syndrome; ischemia-reperfusion injury; acute inflammation; bacterial infection; vaccine; parasitic worm infection; antihelminic.
                                                                                                                                                                                                                                                 US5919900-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Canine hookworm neutrophil inhibitory factor isoform clone IFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY23592 standard; Protein; 274 AA.
                                     10-NOV-1993;
26-MAY-1995;
                                                                                                                                                                                                             06-JUL-1999
(CORV-) CORVAS INT INC
                                                                                                                                                                         26-MAY-1995;
                                                                                                                                                                                                                                                                                       Ancylostoma caninum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202 TTIHVVCHYPKINKTEGEPIYKVGTPCDDCSEY 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 --- HVVCQYGPEAKGDGKTIYEEGAPCSRCSDY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 EAFNLNKTEEGEEVLYRSNHDISNFANLAWDAREKFGCAVVNCPLGEIDDETIHDGETYA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39 SKMRTMVYDCTLEEKAYKSAEKCSEE---PSSEEENVDVFSAATLNI---PLEAGNSWWS 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 EIFEL----RGK--YYNKNGKTSNIANMVWDSHDKLGCAVVDC------SGKT-- 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 SKMRYLEYDCEAEKSAYMSARNCSDSSSPPEGYDENKYIFENSN-NISEAALKAMISWAK 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 MCQQNGTEMPDFNDSIRLQFLAMHNGYRSKLALGHISITEESESDDDDDFGFLPDFAPRA 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 LCQQR----EKLDDDMREMFTELHNGYRAAFARNY------KT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     274 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                   93US-0173510.
92US-0881721.
92US-0996972.
93US-0060433.
93US-0151064.
95US-0450497.
                                                                                                                                                                       9505-0450497.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25,
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Best Local (
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PAXRAPR PRACTO

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The specification describes mutant Neutrophil Inhibitory Factors (NIFS), CC where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197, CC or 223 in the wild type sequence (see ANY23591) is replaced by a Gln Cresidue. NIFS may be useful for treating shock, stroke, acute and chronic allograft rejection, vasculitie, autoimmune diabetes, rheumatoid CC arthritis, inflammatory skin diseases, inflammatory bowel disease, adult Crespiratory distress syndrome (ANDS), ischemia-reperfusion injury CC following myocardial inferction, and acute inflammation caused by bacterial infection such as sepsis or bacterial meningitis. NIFS or NIF CF following myocardial inferction, and acute inflammation caused by CC following myocardial inferction, and acute inflammation of a mammalian or inferction of a mammalian or inferction of a mammalian or compounds. Other worm, as antihelminic agents, and in the detection and isolation of NIF from tissue homogenates, cloned cells etc. NIFS may CC compounds. Other NIF agonists and inhibitors may also be used as antihelminic agents. AAY23592-98 represent isoform clones of canine or hockworm NIF.
                                                                     Neutrophil inhibitory factor: NIF; mutant; shock; stroke; allograft rejection; vasculitis; autoimmune diabetes; ARDS; rheumatoid arthritis; inflammatory skin disease; myocardial infarction; inflammatory bowel disease; adult respiratory distress syndrome; ischemia-reperfusion injury; acute inflammation; bacterial infection; vaccine; parasitic worm infection; antihelminic.
Ancylostoma caninum.
                                                                                                                                                                                                                                                                                                                                                            Neutrophil inhibitory factor clone 1FL.
                                                                                                                                                                                                                                                                                                                                                                                                                                           03-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY23591 standard; Protein; 274 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-403975/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inflammatory responses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214 NKTEGOPIYKVGTPCDDCSEY 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 GYLYRSNHDISNFANLAWDAREKFGCAVVNCPLGEIDDETNHDGETYATTIHVVCHYPKI 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 EEKAYKSAEKCSEE---PSSEEENVDVFSAATLNI---PLEAGNSWWSEIFEL-----R 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35 NDSIRLQFLAMHNGYRSKLALGHISITEESESDDDDDFGFLPDFAPRASKMRYLEYDCEA 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  274 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 274;
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The specification describes mutant Neutrophil Inhibitory Factors (NIFS), CC where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197, CC or 223 in the wild type sequence (see ANZ2591) its replaced by a Gln cc residue. NIFS may be useful for treating shock, stroke, acute and cc chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid CC arthritis, inflammatory skin diseases, inflammatory bowel disease, adult crespiratory distress syndrome (ARDS), ischemia-reperfusion injury CC following myocardial infarction, and acute inflammation caused by a CC following myocardial infarction, and acute inflammation caused by a CC fragments may be used as vaccines against parasitic worm infection. CC fragments may be used as vaccines against parasitic worm infection of a mammalian const by a parasitic worm, as antihabminic agents, and in the detection cand isolation of NIF from tissue homogenates, cloned cells etc. NIFs may compounds. Other NIF agonists and inhibitors may also be used as compounds. Other NIF agonists and inhibitors may also be used as cantine hookworm compounds. Other NIF agonists and inhibitors may also be used as cantine hookworm.
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Best Local S
Matches 69
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11-MAY-1993;
10-NOV-1993;
26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-403975/34.
N-PSDB; AAX85535.
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11-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Foster DL, Moyle M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
             13-AUG-2002 (first entry)
                                                                    AAU97699;
                                                                                                                       AAU97699 standard; Protein;
                                                                                                                                                                                                                                                             214 NKTEGOPIYKVGTPCDDCSEY 234
                                                                                                                                                                                                                                                                                                                143 AKGDGKTIYEEGAPCSRCSDY 163
                                                                                                                                                                                                                                                                                                                                                                   154 GYLYRSNHDISNFANLAWDAREKFGCAVVNCPLGEIDDETNHDGETYATTIHVVCHYPKI 213
                                                                                                                                                                                                                                                                                                                                                                                                                          99 GKVYNKNGKTSNIANMVWDSHDKLGCAVVDC-----SGKT-----HVVCQYGPE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 EEKAYKSAEKCSEE---PSSEEENVDVFSAATLNI---PLEAGNSWWSEIFEL-----R 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35 NDSIRLQFLAMHNGYRSKLALGHISITEESESDDDDDDFGFLPDFAPRASKMRYLEYDCEA 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 DDDMREMETELHNGYRAAFARNY------------KTSKMRTMVYDCTL 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95 EKSAYMSARNCSDSSSPPEGYDENKYIFENSN-NISEAALKAMISWAKEAFNLNKTKEGE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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92US-0881721.
92US-0996972.
93US-0060433.
93US-0151064.
95US-0450497.
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34.3%; Pred. No. 1.1e-21;
tive 23; Mismatches 57; Indels 52; Gaps
                                                                                                                              274
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                                                                                                                                                                                                                                                                                                                                               The present invention relates to a new method for treating copathophysiological conditions involving neutrophils. The method of the convention involves administering to a subject simultaneously/separately/ sequentially Neutrophil inhibitory Factor (NIF) and another conventially Neutrophil inhibitory Factor (NIF) and another convention is salt, where the agents are present in amounts that render the combination of the 2 or more agents effective in treating the combination of the 2 or more agents effective in treating the combination of the 2 or more agents effective in treating the convention of the 2 or more agents effective in treating the convention of the 2 or more agents effective in treating the conventions involving neutrophils. The combination of the 1 state one neutrophil inhibitory Factor (NIF) and at least one other convented to a medicament of the treatment of the treatment of the treatment of the useful in the manufacture of a medicament for the treatment of the treatment of conthophysiological conditions involving neutrophils. In particular, the candor reperfusion injury, post-ischaemic demage conditions involving neutrophils is ischaemic damage cand/or reperfusion injury, post-ischaemic cerebral inflammation conversed to the present amino acid sequence represents the canine (dog) hookworm conversed to the present amino acid sequence represents the canine (dog) hookworm conversed to the present amino acid sequence represents the canine (dog) hookworm conversed to the present amino acid sequence represents the canine (dog) hookworm conversed to the present amino acid sequence represents the canine (dog) hookworm conversed to the present amino acid sequence represents the canine (dog) hookworm conversed to the present amino acid sequence represents the canine (dog) hookworm conversed to the present amino acid sequence represents the canine (dog) hookworm conversed to the present amino acid sequence represents the canine (dog) hookworm conversed the present amino acid sequence represents the canine th
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Best Local S
Matches 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Canine hookworm Neutrophil Inhibitory Factor (NIF) protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of a combination of at least one Neutrophil Inhibitory Pactor and at least one other neuroprotective or thrombolytic/fibrinolytic agent for treating e.g. stroke, traumatic head injury or post-ischaemic cerebral inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-OCT-2000; 2000GB-0025473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brearley CJ, Butler P, (MacIntyre F, McElroy AB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PFIZ ) PFIZER LTD. (PFIZ ) PFIZER INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-OCT-2001; 2001WO-IB01936.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Fig 2; 110pp; English.
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                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                  69;
                                                                                                                                     14 DDDMREMFTELHNGYRAAFARNY------------KTSKMRTMVYDCTL 50
51 EEKAYKSAEKCSEE---PSSEEENVDVFSAATLNI---PLEAGNSWWSEIFEL------R 98
                                                                                  35 NDSIRLQFLAMHNGYRSKLALGHISITEESESDDDDDFGFLPDFAPRASKMRYLEYDCEA 94
                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                274 AA;
                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label- Signal_peptide
18..274
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1..17
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/note= "Specifically claimed in claim 2"
                                                                                                                                                                                            29.1%; Score 290; DB 23; Length 274; 34.3%; Pred. No. 1.1e-21; tive 23; Mismatches 57; Indels 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chahwala SB,
B, McHarg AD;
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Chopp M, Krams M,

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Indels 52;

Gaps

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Okediadi CA,

Pias

SJ;

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  23-AUG-2000;
                                    15-AUG-2001; 2001WO-US25733
                                                                                                             WO200216584-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE20890 standard;
                                                                                                                                                                                                                                                                          Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiinflammatory; vasotropic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NKTEGOPIYKVGTPCDDCSEY 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AKGDGKTIYEEGAPCSRCSDY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVLYRSNHDISNFANLAWDAREKFGCAVVNCPLGEIDDETNHDGETYATTIHVVCHYPKI 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GKVYNKNGKTSNIANMVWDSHDKLGCAVVDC-----SGKT-----HVVCQYGPE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKSAYMSARNCSDSSSPPEGYDENKY I FENSN-NI SEAALKAMI SWAKEAFNLNKTKEGE
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  2000US-0644942
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                                                                                                                                                                                                     /note- "
251..261
                                                                                                                                                /note=
267..27
/note=
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177..1
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77..90
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36..50
                                                                                                                                                                                                                                            224..236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'label- Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein; 274 AA
                                                                                                                                                                                                                                                                              ..189
                                                                                                                                                                   . 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - Mature_NIF1_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "D-67 peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "D-85 peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "N-terminal region"
                                                                                                                                                "K-48, T-22-10 peptides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "D-53, D54 peptides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "T-13 peptide"
                                                                                                                                                                                  "D-61 peptide"
                                                                                                                                                                                                                                                         "K-46B peptide"
                                                                                                                                                                                                                                                                                           "D-96 peptide"
                                                                                                                                                                                                                                                                                                                                "K-50A peptide'
                                                                                                                                                                                                                                                                                                                                                                                                       "T-20 peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                         "D-102 peptide"
                                                                                                                                                                                                                    "T-15-6 peptide"
                                                                                                                                                                                                                                                                                                                                                                  "K-34A peptide"
RESULT 20
AAY23599
ID AAY23
XX
AC AAY23
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DT 03-SE
XX
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DE Prote
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KW Neutr
KW allog
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method for the preparation of neutrophil CC inhibitory factor (NIF) comprising growing a cell line expressing NIF CC in an animal component-free medium salected from inoculum growth medium. CC endture. The method is useful for preparation of NIF. Animal component-CC free production growth medium is useful for preparation of recombinant CC production growth medium is useful for preparation of recombinant CC production growth medium is useful for preparation. Of recombinant CC productions characterised by abnormal neutrophil activation, for treating CC shock, stroke, acute and chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid arthritis, head trauma, inflammatory CC skin diseases, inflammatory bowel disease, adult respiratory distress cynfrome (ARDS), ischaemia-reperfusion injury following myocardial infarction, in which neutrophil infiltration and activation has been complicated and acute inflammation caused by bacterial infection, such as espsis or bacterial meningitis. NIF is also useful as diagnostic agents. CC sepsis or bacterial meningitis. NIF is also useful as diagnostic agents. CC antagonists for their ability to affect NIF minics or to detect NIF creeptor, as a vaccine against parasitic worm infections in mammals, and CC is Ancylostoma canium NIF1 protein encoded by pEE14/NIF1cr insert DNA.
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Preparing Neutrophil Inhibitory Factor for treating shock, by growing cell line expressing the factor in animal component-free medium such inoculum growth medium, production growth medium or nutrient feed -
Neutrophil inhibitory factor; NIF; mutant; shock; stroke, allograft rejection; vasculitis; autoimmune diabetes; ARI
                                                   Protein encoded by two-cistron Met-NIF expression cassette
                                                                                          03-SEP-1999 (first entry)
                                                                                                                              AAY23599;
                                                                                                                                                                 AAY23599 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Fig 1; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pluschkell SB, Geldart RW, Zhu MM, Hawrylik SJ, Moyle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2001; 2001US-0797410
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(CORV-) CORVAS INT :
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DB; AAD33306.
                                                                                                                                                                                                                                                                              143 AKGDGKTIYEEGAPCSRCSDY 163
                                                                                                                                                                                                                                                                                                                                154
                                                                                                                                                                                                                                                           214 NKTEGOPIYKVGTPCDDCSEY
                                                                                                                                                                                                                                                                                                                                                                  99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 34.3
59; Conservative
                                                                                                                                                                                                                                                                                                                                                   GKYYNKNGKTSNIANMYWDSHDKLGCAVYDC------SGKT-----HVYCQYGPE 142
                                                                                                                                                                                                                                                                                                                                                                                                                            GVLYRSNHDISNFANLAWDAREKFGCAVVNCPLGEIDDETNHDGETYATTIHVVCHYPKI 213
                                                                                                                                                                                                                                                                                                                                                                                                         EKSAYMSARNCSDSSSPPEGYDENKYIFENSN-NISEAALKAMISWAKEAFNLNKTKEGE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NDSIRLQFLAMHNGYRSKLALGHISITEESESDDDDDDFGFLPDFAPRASKMRYLEYDCEA 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              274 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 290; DE; Pred. No. 1.16
23; Mismatches
                                                                                                                                                                 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>,.</u> 9.
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l.1e-21;
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57;

Indels

52;

Gaps

Length 274;

ARESULT 19
AREZOLT 19
AREZO
XX AREZO
XX AREZO
XX OL-JU
XX PEEL4
XX Neutr
KW PASCA
XW Infoca
KW I

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The specification describes mutant Neutrophil Inhibitory Factors (NIFs), CC where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197, CC or 223 in the wild type sequence (see ANZ3351) is replaced by a Gln CC residue. NIFs may be useful for treating shock, stroke, acute and chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid cc arthritis, inflammatory skin diseases, inflammatory bowel disease, adult respiratory distress syndrome (ARDS), ischemia-reperfusion injury bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF CC following myocardial infarction, and acute inflammation caused by acterial infection such as sepsis or bacterial meningitis. NIFs or NIF CC fragments may be used as vaccines against parasitic worm infection and instrumental parasitic worm, as antihelminic agents, and in the detection cand isolation of NIF from tissue homogenates, cloned cells etc. NIFs may be useful for the detection of NIF mimics or antagonists in other CC compounds. Other NIF agonists and inhibitors may also be used as antihelminic agents. The present sequence is encoded by a two-cistron CC Met-NIF expression cassette of Pma5-NII/3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-DEC-1993;
11-MAY-1992;
24-DEC-1992;
11-MAY-1993;
10-NOV-1993;
26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mutant Neutrophil Inhibitory Factors useful for treating inflammatory conditions and especially to prevent or decinflammatory responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Foster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORV-) CORVAS INT INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rheumatoid arthritis; inflammatory skin disease; myocardial infarction; inflammatory bowel disease; adult respiratory distress syndrome; ischemia-reperfusion injury, acute inflammation; bacterial infection; raccine; parasitic worm infection; antihelminic.
                                                                                                                    169
                                                                                                                                                                                                                          110
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DB; AAX85536.
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                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity 34.3
69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20; Fig 15A-D; 131pp; English.
            NKTEGQPIYKVGTPCDDCSEY
                                                       AKGDGKTIYEEGAPCSRCSDY 163
                                                                                                     GVLYRSNHDISNFANLAWDAREKFGCAVVNCPLGEIDDETNHDGETYATTIHVVCHYPKI 228
                                                                                                                                       GKYYNKNGKTSNIANMYWDSHDKLGCAVVDC-----SGKT-----SGKT-----HVVCQYGPE 142
                                                                                                                                                                                                       EKSAYMSARNCSDSSSPPEGYDENKYIFENSN-NISEAALKAMISWAKEAFNLNKTKEGE
                                                                                                                                                                                                                                            EEKAYKSAEKCSEE---PSSEEENVDVFSAATLNI---PLEAGNSWWSEIFEL-----R
                                                                                                                                                                                                                                                                                                                                                              DDDMREMFTELHNGYRAAFARNY------50
                                                                                                                                                                                                                                                                                                             NDSIRLQFLAMHNGYRSKLALGHISITEESESDDDDDFGFLPDFAPRASKMRYLEYDCEA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    289 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Moyle M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93US-0173510.
92US-0881721.
92US-0996972.
93US-0060433.
93US-0151064.
95US-0450497.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 29.18;
                                                                                                                                                                                                                                                                                                                                                                                                                            23;
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 290; DB 20;
Pred. No. 1.2e-21;
3; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 289;
                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                decrease
                                                                                                                                                                                                                                                                                                                                                                                                                     52;
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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NDSIRLQFLAMHNGYRSKLALGHISITEESESDDDDDDFGFLPDFAPRASKMRYLEYDCEA

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RESULT 21
AAX23077
ID AAX23
AC AAX23
AC AAX23
AX O3-SE
XX Neutr
KW Neutr
KW 150fla
KW 150fla
KW 150fla
KW 160fla
KW 23-DE
PR 11-MA
PR 10-MA
PR 1
                                                                                                                                                                                                                                          The specification describes mutant Neutrophil Inhibitory Factors (NIFs), CC where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197, CC where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197, CC or 223 in the wild type sequence (see AAY23591) is replaced by a Gln CC chronic allograft rejection, vasculitis, shock, stroke, acute and CC chronic allograft rejection, vasculitis, antoinmune diabetes, rheumatoid CC arthritis, inflammatory skin diseases, inflammatory bowel disease, adult Crespiratory distress syndrome (ARDS), ischemia reperfusion injury CC pacterial infection such as sepsis or bacterial meningitis. NIFS or NIF CC fragments may be used as vaccines against parasitic worm infection. CC fragments may be useful for detecting infection of a mammalian can be useful for the detection of NIF minics or antagonists in other CC compounds. Other NIF agonists and inhibitors may also be used as compounds. Other NIF agonists and inhibitors may also be used as compounds. Other NIF agonists and inhibitors may also be used as compounds. Other NIF agonists and inhibitors may also be used as compounds.
                                                                                      Query Match
Best Local S
Matches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-DEC-1993;
11-MAY-1992;
11-MAY-1992;
24-DEC-1992;
11-MAY-1993;
10-NOV-1993;
26-MAY-1995;
                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 21; Fig 16A-V; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mutant Neutrophil Inhibitory Factors useful for treating inflammatory conditions and especially to prevent or decrease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neutrophil inhibitory factor; NIF; mutant; shock; stroke; allograft rejection; vasculitis; autolimune diabetes; ARDS; rheumatoid arthritis; inflammatory skin disease; myocardial infarctio inflammatory bowel disease; adult respiratory distress syndrome; ischemia reperfusion injury; acute inflammation; bacterial infection; vaccine; parasitic worm infection; antihelminic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CORV-) CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ancylostoma canium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canine hookworm neutrophil inhibitory factor AcaNIF19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ŗ,
                                                                               Similarity 34.: 69; Conservative
DDDMREMFTELHNGYRAAFARNY------KTSKMRTMVYDCTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Moyle M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 responses
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92US-0881721.
92US-0996972.
93US-0060433
93US-0151064.
95US-0450497.
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                                                                                                                 28.8%;
                                                                                  22;
                                                                           Score 287; DB
Pred. No. 2.3e
22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    274
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                                                                                                       .3e-
                                                                    1 20;
-21;
58;
                                                                                                                                      Length
                                                                               Indels
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                                                                               52;
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RESULT 22
AAR52985
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                                                                                               Query Match
Best Local S
Matches 75
                                                                                                                                                                  A canine hookworm cDNA library was screened with a probe amplified using primers 30.2 and 43.3.RC(AAQ52476 and AAQ52477, respectively) which were based on sequences of isolated NIF peptide fragments. Seven of the 120 positive clones were isolated for sequence analysis. One isolate, designated clone IFL, encoded and 85 nucleotide open reading frame (AAQ52475). The other clones contained partial ORFs and encoded partial NIF polypeptides (see AAR52985-R52990) which are thought to represent six NIF isoforms that are significantly similar to, but not identical to, the prototypical NIF-IFL polypeptide (AAR42488).
                                                                                                                                                                                                                                                                                                                   New neutrophil inhibitory factor from parasitic worms - for preventing and treating inflammation, also derived nucleic vectors, transformed hosts and antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neutrophil inhibitory fac
nematode; parasitic worm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Canine hookworm Neutrophil Inhibitory Factor isoform
                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                               Example 10; Fig 9; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                        WPI; 1993-386208/48.
                                                                                                                                                                                                                                                                                                                                                                                                                        (CORV-) CORVAS INT INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR52985 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143
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97
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                    37
                                              37
                                                                                                                                                                                                                                                                                                                                                                                                DL,
                                                              Similarity
75; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AKGDGKTIYEEGAPCSRCSDY 163
| :|: ||: | || || ||
NKTEGQPIYKVGTPCDDCSGY 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKYYKKIGKTSAILAMYMDSHDKLGCAVVDC-----SGKT----HYVCQYGPE 142
              KTSKMRTMYYDCTLEEKAYKSAEKCSEEPSSEE---ENV------DVFSAATLNIPLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EKSAYMSARNCSDSSSPPEGYDENKYIFENSN-NISEAALKAMISWAKEAFNLNKTEEGE
 RASKMRYLKYDCEAEKSAYESAKKCQTTASSWEKYDENLQVIEDPKDINHAA-----LKA 151
                                                 EHDPTCPQNGEKMEKGFDDAIRLKFLAMHNGYRSRLALGHVSITEESEDYDLDYDLLYAP
                                                                                        28.7%;
milarity 36.9%; 1
Conservative 22;
                                                                                                                                                 234 AA;
                                                                                                                                                                                                                                                                                                                                                                                               Moyle M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                               92US-0881721.
92US-0996972.
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                                                                                                                                                                                                                                                                                                                                                                                                Vlasuk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                factor; NIF; glycoprotein; endoparasite;
orm; canine hookworm; peritoneal inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234
                                                                                              Score 286.5; DB 14,
Pred. No. 2.1e-21;
2; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                               GP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₹
                                                                                                                       DB 14;
                                                                                               Indels
                                                                                                                       Length 234;
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                                                                                                                                                                                                                                                                                                                                   acid,
                                                                                               45;
                                                                                               Gaps
                                                                                                                                                                                                                                              Seven
                       86
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ARESULTY 23
ARAY23608
ID ARY23
AC ARY23
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                                                 The specification describes mutant Neutrophil Inhibitory Factors (NIF8), CC where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197, CC or 223 in the wild type sequence (see AAY23591) is replaced by a Gin C residue. NIFs may be useful for treating shock, stroke, acute and C chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid arthritis, inflammatory skin diseases, inflammatory bowel disease, adult respiratory distress syndrome (ARDS), ischemia-reperfusion injury CC following myocardial infarction, and acute inflammation caused by acterial infection such as sepsis or bacterial meningitis. NIFs or NIF CC fragments may be used as vaccines sgainst parasitic worm infection. CC host by a parasitic worm, as antihelminic agents, and in the detection host by a parasitic worm, as antihelminic agents, and in the detection of NIF from tissue homogenates, cloned cells etc. NIFs may CC compounds. Other NIF agonists and inhibitors may also be used as compounds. Other NIF agonists and inhibitors may also be used as compounds. Other NIF agonists and inhibitors may also be used as compounds. Other NIF agonists and inhibitors may also be used as compounds. Other NIF agonists and inhibitors may also be used as
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11-MAY-1993;
10-NOV-1993;
26-MAY-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US5919900-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Foster DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CORV-) CORVAS INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-DEC-1993;
11-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAY-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inflammatory responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rheumatoid arthritis; inflammatory skin disease; myocardial infarction; inflammatory bowel disease; adult respiratory distress syndrome; ischemia reperfusion injury, acute inflammation; bacterial infection; raccine; parasitic worm infection; antihelminic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1999-403975/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEAKGDGKTIYEEGAPCSRCSDY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moyle M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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92US-0881721.
92US-0996972.
93US-0060433.
93US-0151064.
95US-0450497.
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RESULT 24
AAY23602
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                                                                                                                                                                                                                                                                                                                    23-DEC-1993;
11-MAY-1992;
24-DEC-1992;
11-MAY-1993;
10-NOV-1993;
The specification describes mutant Neutrophil Inhibitory Factors (NIFs), where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197, or 223 in the wild type sequence (see AAY23591) is replaced by a Gin residue. NIFs may be useful for treating shock, stroke, acute and chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid arthritis, inflammatory skin diseases, inflammatory bowel disease, adult
                                                                                                                                               Mutant Neutrophil Inhibitory Factors useful for treating inflammatory conditions and especially to prevent or decrease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neutrophil inhibitory factor, NIF; mutant; shock; stroke; allograft rejection; vasculitis; autoimmune diabetes; ARDS; rheumatoid arthritis; inflammatory skin disease; myocardial infarction; inflammatory bowel disease; adult respiratory distress syndrome; ischemia reperfusion injury; acute inflammation; bacterial infection; vaccine; parasitic worm infection; antihelminic.
                                                                                                       Example 21; Fig 16A-V; 131pp; English.
                                                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                                                           Foster DL,
                                                                                                                                                                                                                                                                                                         26-MAY-1995;
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                                                                                                                                                                                                                                                                          (CORV-) CORVAS INT INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY23602 standard; Protein; 263 AA
                                                                                                                                        inflammatory responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY23602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                 1999-403975/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 EGEGVLYRSNHDISNFANLAWDTREKFGCAVVNCPLGEIDGTTIDDGETYATTIHVVCHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 PKMNKTEGEPIYKVGKPCRDCSEY 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 GPEAKGDGKTIYEEGAPCSRCSDY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 DDDMREMETELHNGYRAAFARNY------KTSKMRTMVYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98 -- RGKYYNKNGKTSNIANMYWDSHDKLGCAVVDC------SGKT-----HVVCQY 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48 CTLEEKAYKSAEKCSEE----PSSEEENVDVFSAATLNI----PLEAGNSWWSEIFEL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 NDSIRLQFLAMHNGYRSKLALGHISITDESESESDDEYDYWYAPTAYAPTASKMRYLEYD
                                                                                                                                                                                                   AAX85539.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CEAEKSAYMSARNCSDSSSPPEGYDENKYIFENSN-NISEAALKAMISWAKEAFNLNKTE 153
                                                                                                                                                                                                                                           Moyle M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                 93US-0173510
92US-0881721
                                                                                                                                                                                                                                                                                                      95US-0450497
                                                                                                                                                                                                                                                                                                                                                                                                          9508-0450497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 284.5;
Pred. No. 4.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .1e-21;
es 58; Indels 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR52988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88888888888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
A canine hookworm cDNA library was screened with a probe amplified using primers 30.2 and 43.3.RC(AAQ52476 and AAQ52477, respectively) which were based on sequences of isolated NIF peptide fragments. So
                                                                                                                                                                                                  New neutrophil inhibitory factor from parasitic worms - for preventing and treating inflammation, also derived nucleic acid, vectors, transformed hosts and antibodies
                                                                                                                                                       Example 10;
                                                                                                                                                                                                                                                                                                                                                          WPI; 1993-386208/48.
                                                                                                                                                                                                                                                                                                                                                                                                                         Foster DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CORV-) CORVAS INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-MAY-1992;
24-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09323063-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neutrophil inhibitory factor; NIF; glycoprotein; endoparasite; nematode; parasitic worm; canine hookworm; peritoneal inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Canine hookworm Neutrophil Inhibitory Factor isoform 3FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    respiratory distress syndrome (ARDS), ischemia-reperfusion injury following myocardial infarction, and acute inflammation caused by bacterial infection such as sepsis or bacterial meninglis. NIFs or NIF fragments may be used as vaccines against parasitic worm infection. Anti-NIF antibodies may be useful for detecting infection of a mammalian host by a parasitic worm, as antihelminic agents, and in the detection and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may be useful for the detection of NIF mimits or antagonists in other compounds. Other NIF agonists and inhibitors may also be used as antihelminic agents. AAY23600-10 represent canine hookworm NIF proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ancylostoma caninum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR52988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR52988 standard; Protein; 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TESO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    199 IPKINKTEGEPIYKVGTPCDDCSEY 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 YGPEAKGDGKTIYEEGAPCSRCSDY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139 NKTGEGVLYRSNLTISNFANLAWDTREKFGCAVVNCPLGEIDADIYDEETYATTIHVVCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 ----RGKYYNKNGKTSNIANMVWDSHDKLGCAVVDC-----SGKTHVVCQ 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 CEAEKSAYMSARNCSDSSSPPEGYDENKYIFENSNNISEAARLAI-----LSWAKEAFDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48 CTLEEKAYKSAEKCSEE----PSSEEENVDVF-----SAATLNIPLEAGNSWWSEIFEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 NDSIRLQFLAMHNGYRSKLALGHISITDESESESDDEYDYWYAPTAYAPTASKMRYLEYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 AA;
                                                                                                                                               Fig 9; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                     Moyle M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        920S-0881721
920S-0996972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93WO-US04502
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                                                                                                                                                                                                                                                                                                                                                                                                                     Vlasuk GP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97
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RESULT 26
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Best Local
                                                                                                                                                                                                                                                           23-DEC-1993;
11-MAY-1992;
24-DEC-1992;
11-MAY-1993;
10-NOV-1993;
26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neutrophil inhibitory factor; NIF; mutant; shock; stroke; allograft rejection; vasculitis; autoimmune diabetes; ARDS; rheumatoid arthritis; inflammatory skin disease; myccardial inflammatory bowel disease; adult respiratory distress syndischemia-reperfusion injury; acute inflammation; bacterial; vaccine; parasitic worm infection; antihalminic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the 120 positive clones were isolated for sequence analysis one isolate, designated clone IFL, encoded an 825 nucleotide open reading frame (AAQ52475). The other clones contained partial ORFs and encoded partial NIF polypeptides (see AAR52885-B52990) which are thought to represent six NIF isoforms that are significantly similar to, but not identical to, the prototypical NIF-IFL polypeptide (AAR42488).
                                                             Mutant Neutrophil Inhibitory Factors useful for treating inflammatory conditions and especially to prevent or decrease
                                                                                                                                 WPI; 1999-403975/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US5919900-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ancylostoma caninum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Canine hookworm neutrophil inhibitory factor isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-SEP-1999
Example 10; Fig 9A-E; 131pp; English
                                                                                                                                                                            Foster
                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY23596 standard; Protein; 224 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                             inflammatory responses
                                                                                                                                                                                                                     (CORV-) CORVAS INT INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210 NKTEGOPIYKVGKPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150
                                                                                                                                                                          DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 DDDMREMFTELHNGYRAAFARNY--------KTSKMRTMVYDCT 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AKGDGKTIYEEGAPC 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVLYRSNHDISNFANLAWDTREKFGCAVVNCPLGEIDGTTIHDGETYATTIHVVCHYPKM 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AEKSAYMSARNCSDSSSPPEGDENKYIFENSN-NISEAALKAMISWAKEAFNLNKTEEGE 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEEKAYKSAEKCSE--EPSSEEENVDVFSAATLNI---PLEAGNSWWSEIFEL-----R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NDSIRLQFLAMHNGYRSKLALGHISITDESESESDDEYDYWYAPTAPTASKMRYLEYDCE 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224 AA;
                                                                                                                                                                          Moyle M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                           93US-0173510
92US-0881721
92US-099572
93US-0060433
93US-0151064
95US-0450497.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 266; DB 14;
Pred. No. 2.7e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infarction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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RESULT 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The specification describes mutant Neutrophil Inhibitory Factors (NIFS), CC where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197, CC or 223 in the wild type sequence (see ANY23591) is replaced by a Gin C chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid CC arthrilis, inflammatory skin diseases, inflammatory bowel disease, adult C respiratory distress syndrome (ARDS), ischemia-reperfusion injury CC following myocardial inferction, and acute inflammation caused by CC fragments may be used as vaccines against parasitic worm infection in CC fait NIF antibodies may be useful for detecting infection of a mammalian CC host by a parasitic worm, as antihelminic agents, and in the detection and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may be useful for detecting agents, and in the detection of the useful for the detection of NIF minics or antagonists in other C compounds. Other NIF agonists and inhibitors may also be used as antihelminic agents. AAY23592-98 represent isoform clones of canine CC hockworm NIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                          Key
Peptide
                                                                                                                                                                                                                                                                         Ancylostoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                          (UYYA ) UNIV YALE.
                                                         10-APR-1995;
                                                                                       10-APR-1996;
                                                                                                                      17-OCT-1996.
                                                                                                                                                  WO9632479-A1.
                                                                                                                                                                                               Protein
                                                                                                                                                                                                                                                                                                     Ancylostoma secreted protein; ASP-1; hookworm; vaccine.
                                                                                                                                                                                                                                                                                                                                Ancylostoma secreted protein ASP-1 (pro-form).
                                                                                                                                                                                                                                                                                                                                                                17-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                 AAW04321;
                                                                                                                                                                                                                                                                                                                                                                                                                             AAW04321 standard; Protein; 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 AKGDGKTIYEEGAPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210 NKTEGQPIYKVGKPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 DDDMREMFTELHNGYRAAFARNY------49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 AEKSAYMSARNCSDSSSPPEGDENKYIFENSN-NISEAALKAMISWAKEAFNLNKTEEGE 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 NDSIRLQFLAMHNGYRSKLALGHISITDESESESDDEYDYWYAPTAPTASKMRYLEYDCE 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVLYRSNHDISNFANLAWDTREKFGCAVVNCPLGEIDGTTIHDGETYATTIHVVCHYPKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GKVYNKNGKTSNIANMVWDSHDKLGCAVVDC-----SGKT-----HVVCQYGPE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEEKAYKSAEKCSE--EPSSEEENVDVFSAATLNI---PLEAGNSWWSEIFEL------R 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             224 AA;
Hotez PJ,
                                                                                                                                                                                                                                                                          caninum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                         9508-0419414.
                                                                                       96WO-US04821.
                                                                                                                                                                                          /label- Sig_peptide
                                                                                                                                                                               /label= Mat_protein
                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.7%;
Jones BF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 266; DB
Pred. No. 2.7e
21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52;
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Query Match 26.6
Best Local Similarity 32.5
Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ancylostoma secreted protein ASP-1 is secreted by canine hookworm larvae as they change from the free-living stage to the parasitic stage. The amino acid sequence of the ASP-1 pro-form (AAW04321) was detd. from a cDNA clone (AAW38465) obtd. from an Ancylostoma caninum is larvae cDNA library. ASP-1 represents a family of proteins (see also AAW0432-23) that are highly immunogenic in experimental animals. Recombinant ASP proteins can be produced in a variety of hosts. They can be used in vaccines for hookworm, in the diagnosis of hookworm infection, or to raise antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-477130/47.
N-PSDB; AAT38466.
                                                                                                                                                                                                                                                                        17-JAN-1997 (first entry)
                                                                                                                                                                                                                                                                                               AAW04322;
                                                                                                                                                                                                                                                                                                                    AAW04322 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 42-43; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ancylostoma caninum secreted protein \cdot useful as antigen for hookworm vaccine prodn.
                                                                                                             10-APR-1995;
                                                                                                                                                           17-OCT-1996.
                                                                                                                                                                                                      Ancylostoma caninum
                                                                                                                                                                                                                           Ancylostoma secreted protein; ASP-2; hookworm; vaccine
                                                                                                                                                                                                                                                Ancylostoma secreted protein ASP-2 type I.
                                                                 Hawdon JM, Hotez PJ,
                                                                                                                                    10-APR-1996;
                                                                                                                                                                                W09632479-A1
                                 WPI; 1996-477130/47.
N-PSDB; AAT38467.
                                                                                       (UYYA ) UNIV YALE.
Ancylostoma caninum secreted protein - hookworm vaccine prodn.
                                                                                                                                                                                                                                                                                                                                                                             407
                                                                                                                                                                                                                                                                                                                                                                                                                                     100 KYYNKNG-KTSNIANMYWDSHDKLGCAVVDCSGKTHVVCQYGPEAKGDGKTIYEEGAPCS 158
                                                                                                                                                                                                                                                                                                                                                                                               159 RCSDYGAGVTC 169
                                                                                                                                                                                                                                                                                                                                                                                                                       347 ALWNRPGMQIGHYTQMAWDTTYKLGCAYVFCNDFTFGVCQYGPGGNYMGHVIYTMGQPCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                227
                                                                                                                                                                                                                                                                                                                                                                            QCS---PGATC 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HGNKCVYQHSHGEDRPGLGENIYKTSVLKFDKNKAAKQASQLWWNELKEFGVGPSNVLTT 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAEKCSEEPSSEEE----NVDVFSAATLNI-----PLEAGNSWWSEIFE-----LRG 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CPSNTGMTDSVRDTFLSVHNEFRSSVARGLEPDALGGNAPKAAKMLKMVYDCEVEASAIR 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CQQREKLDDDMREMFTELHNGYRAAFARNY-----KTSKMRTMVYDCTLEEKAYK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        424 AA;
                                                                                                               95US-0419414.
                                                                                                                                     96WO-US04821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.6%;
                                                                  Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 265.5;
; Pred. No. 7.46
27; Mismatches
                                                                                                                                                                                                                                                                                                                      218
                                                                  BF;
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            useful as antigen for
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AAW04323
ID AAW04
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Best Local S
Matches 58
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                                                                                           WPI; 1996-477130/47
N-PSDB; AAT38468.
                                                                                                                                                                                                                                                                                                                                  17-JAN-1997
                                                                                                                                                                                                                                                                                                                                                          AAW04323;
                                                                                                                                                                        10-APR-1995;
                                                                                                                                                                                              10-APR-1996;
                                                                                                                                                                                                                    17-0CT-1996.
                                                                                                                                                                                                                                         WO9632479-A1.
                                                                                                                                                                                                                                                               Ancylostoma caninum
                                                                                                                           Hawdon JM, Hotez PJ,
                                                                                                                                                (UYYA ) UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                      207
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58; Conserv
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Ancylostoma secreted protein ASP-2 type I (AAW04322) is secreted by canine hookworm larvae as they begin feeding. Its amino acid sequence was deduced from a cDNA clone (AAT38467) isolated from an Ancylostoma caninum L3 larvae cDNA library. Type I ASP-2 differs from type II ASP-2 (AAW04323) only at amino acid positions 92 and 95. The proteins are members of a family of proteins (see also AAW04321) that are highly immunogenic in experimental animals. Recombinant ASP proteins can be produced in a variety of hosts. They can be used in vaccines for hookworm, in the diagnosis of hookworm infection, or to raise antibodies.
Ancylostoma secreted protein ASP-2 type II (AAW04323) is canine hookworm larvae as they begin feeding. Its amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ancylostoma secreted protein ASP-2 type II.
                                                                               Claim 2; Page 51; 66pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ancylostoma secreted protein; ASP-2; hookworm; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW04323 standard; Protein;
                                                                                                                                        Ancylostoma caninum secreted protein - useful as antigen hookworm vaccine prodn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 SNIANWYWDSHDKLGCAVVDCSGKTHVVCQYGPEAKGDGKTIYEEGAPCSRCSDYGAGVT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 LDDDMREMFTELHNGYRAAFARNY------KTSKMRTMVYDCTLEEKAYKSAEKCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDDDWQNLLCI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GHYTQMVWQESYKLGCYVEWCSSMTYGVCQYSPQGNMMNSLIYEKGNPCTKDSDCGSNAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FAHSHRKGVGENIWMSTAROMDKAQAAQQASDGWFSELAKYGVGQENKLTTQLWNRGVMI 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEPSSEE---ENVDVFSAATLN---IPLEAGNSWWSEIF-----ELRGKVYNKNGKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MTDEAROK FLDVHNSYRSMVAKGQAKDAISGNAPKAAKMKKMIYDCNVESTAMQNAKKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSAG -- EALCV 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26.3%;
ilarity 30.4%;
Conservative 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                            95US-0419414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96WO-US04821.
                                                                                                                                                                                                                                                                                                                         Jones
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Pred. No. 6.7e-19;
B; Mismatches 69;
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RESULT 30
AREI37 30
AREI37 30
AREI37 30
AREI3 XX AREI3
AC AREI3
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Best Loc
Matches
                                                                                                                                                                                                                                                                                                                             (NYBL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anglogenesis; Ov-ASP; therapy; circulatory disorder; vascular disorder; congenital heart disease; myocardial disease; pericardial disease; wart; cerebrovascular ischaemia; veno-occlusive disease; myocardial ischaemia; coronary artery disease; diabetic retinopathy; inflammatory disease; wound healing; duodenal ulceration; rheumatoid arthritis; psoriasis; periodontitis; dermatological; cutaneous malignancy; Kaposi's sarcoma; pyogenic granuloma; cancer; onchocerciasis; River Blindness; neoplasia; vasotropic; cardiant; antiparasitic; opthalmological; dog hookworm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence was deduced from a cDNA clone (AAT38468) isolated from an Ancylostoma caninum L3 larvae cDNA library. Type II ASP-2 differs from type I ASP-2 (AAW04322) only at amino acid positions 92 and 95. The proteins are members of a family of proteins (see also AAW04321) that are highly immunogenic in experimental animals. Recombinant ASP proteins can be produced in a variety of hosts. They can be used in vaccines for hookworm, in the diagnosis of hookworm infection, or to raise antibodies.
                              Inducing angiogenesis in a tissue using from the nematode Onchocera volvulus is vascular disease such as ischemia
                                                                                                                                                                  WPI; 2001-662950/76.
                                                                                                                                                                                                                                Lustigman
                                                                                                                                                                                                                                                                                              (UABR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                 03-APR-2000; 2000US-0541759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-MAR-2001; 2001WO-US09798.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE13070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE13070 standard; Protein; 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                              NEW YORK BLOOD CENT INC.
UNIV CASE WESTERN RESERVE.
UAB RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 30.4
58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDDDWQNLLCI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CSAG--EALCV 215
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                                                                                                                                                                                                                                Pearlman E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.1%;
                                                                                                                                                                                                                                Unnasch TR;
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₹
                                                          the Ov-ASP protein isolated useful to treat circulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108
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RESULT 31
AAR52986
ID AAR52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a method for inducing anglogenesis in a CC tissue. The method comprising contacting the itssue with Ov-ASP. The Ov-ASP molecules are used to treat circulatory or vascular disorders, as molecules are used to treat circulatory or vascular disorders, consential disease, more particularly cerebrovascular ischaemia, veno-coclusive disease, more particularly cerebrovascular ischaemia, veno-coclusive disease or myocardial ischaemia, especially coronary artery coclusive disease or myocardial ischaemia, especially coronary artery coclusive disease or myocardial ischaemia, especially coronary artery coclusive disease. The invention is also used to treat cancer, diabetic retinopathy and inflammatory disease. Anglogenesis is also central to a number of pathological processes, including abnormalities of wound companing the disease such as disease. Anglogenesis is also central to the aling in diseases such as a rheumatorid arthritis, psoriasis and companing the disease such as rheumatorid arthritis, psoriasis and periodontitis; dermatological conditions such as cutaneous malignanty, constituted to treat concocerclasis (River Bindness) or bening or malignant conspirations. The present sequence is Ancylostoma caninum (Ac)-Asp protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
New neutrophil inhibitory factor from preventing and treating inflammation,
                                                     WPI; 1993-386208/48.
                                                                                                                                                            11-MAY-1992;
24-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                    neutrophil inhibitory factor; NIF; glycoprotein; endoparasite;
nematode; parasitic worm; canine hookworm; peritoneal inflamma
                                                                                                                                                                                                                                                                                                                                                                                                          Canine hookworm Neutrophil Inhibitory Factor isoform 1P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR52986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR52986 standard; Protein; 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 1; 37pp; English
                                                                                      Foster DL,
                                                                                                                                                                                                                                                 25-NOV-1993
                                                                                                                                                                                                                                                                                                                   Ancylostoma
                                                                                                                                                                                                                                                                                                                                                                                                                                         02-JUN-1994 (first entry)
                                                                                                                         (CORV-) CORVAS INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 G-KTSNIANMVWDSHDKLGCAVVDCSGKTHVVCQYGPEAKGDGKTIYEEGAPCSRCSDYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 PGATC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165 AGVTC 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 GMQIGHYTQMAWDTTYKLGCAVVFCNDFTFGVCQYGPGGNYMGHVIYTMGQPCSQCS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 YQHSHGEDRPGLGENIYKTSVLKFDKNKAAKQASQLWWNELKEFGVGPSNVLTTALWNRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 LDDDMREMFTELHNGYRAAFARNY-----KTSKMRTMYYDCTLEEKAYKSAEKCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MTDSVRDTFLSVHNERRSSVARGLEPDALGGNAPKAAKMLKMVYDCEVEASAIRHGNKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 33.
61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192 AA;
                                                                                      Moyle M,
                                                                                                                                                                                                                                                                                                                     caninum
                                                                                                                                                            92US-0881721.
92US-0996972.
                                                                                                                                                                                                                93WO-US04502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25.6%;
33.0%;
                                                                                        Vlasuk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26;
                                                                                        GP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 255.5; DB 22;
Pred. No. 2.6e-18;
6; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
    parasitic worms - for
also derived nucleic
                                                                                                                                                                                                                                                                                                                                                      peritoneal inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31;
      acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
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RESULT 32
ARX73594
ID ARX73
XX
AC ARX73
AC ARX73
AX CANIN
XX
CANIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                              23-DEC-1993;
11-MAY-1992;
11-MAY-1992;
24-DEC-1992;
11-MAY-1993;
10-NOV-1993;
26-MAY-1995;
   Mutant Neutrophil Inhibitory Factors useful for treating inflammatory conditions and especially to prevent or dec
                                                                                                                    WPI; 1999-403975/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US5919900-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neutrophil inhibitory factor; NIF; mutant; shock; stroke; allograft rejection; vasculitis; autoimmune diabetes; ARDS; rheumatoid arthritis; inflammatory skin disease; myocardial infarction; inflammatory bowel disease; adult respiratory distress syndrome; ischemia-reperfusion injury; acute inflammation; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A canine hookworm cDNA library was screened with a probe amplified using primers 30.2 and 43.3.R(QAQ52476 and AAQ52477, respectively) which were based on sequences of isolated NIF peptide fragments. Seven of the 120 positive clones were isolated for sequence analysis. One isolate, designated clone IFL, encoded an 825 nucleotide open reading frame (AAQ52475). The other clones contained partial ORFs and encoded partial NIF polypeptides (see AAR32985-R52990) which are thought to represent six NIF isoforms that are significantly similar to, but not identical to, the prototypical NIF-IFL polypeptide (AAR42488).
                                                                                                                                                                                      Foster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ancylostoma caninum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Canine hookworm neutrophil inhibitory factor isoform clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY23594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY23594 standard; Protein; 208
                                                                                                                                                                                                                                                    (CORV-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 10; Fig 9; 114pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 DDDMREMFTELHNGYRAAFARNY--KTSKMRTMYYDCTLEEKAYKSAEKC---SEEPSSE
                                                                                                                                                                                      DĽ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ω
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                                                                                                                                                                                                                                                CORVAS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 36.55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reperiusion injury; acute inflammation; parasitic worm infection; antihelminic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FGCAVVNCPLGKPDAIITDDEENYATAIHVVCHYPKINKTEGQPIYKVGTPCDDCSEY 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EENVDVFSAATLNI---PLEAGNSWWSEIFEL----RGKVYNKNGKTSNIANNVWDSHDK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGCAVVDCS-GK------THVVCQYGPEAKGDGKTIYEEGAPCSRCSDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DENKYIFENSN-NISEAALKAMISWAKEAFNLNKTGEGVLYRSNLTISNFANLAWDTREK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DDD-----YEYGFLPDFAPRASKMRYLEYDCEAEKSAYVSASNCSNISSPPEGY 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transformed hosts and antibodies
                                                                                                                                                                                  Moyle M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 AA;
                                                                                                                                                                                                                                                                                                              93US-0173510.
92US-0881721.
92US-0996972.
93US-0060433.
93US-0151064.
95US-0450497.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9505-0450497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ጅ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
ARESULT 33
AAW37166
ID AAW37
XX
XX
ACC AAW37
XX Haemo
XX Haemo
XX Haemo
XX Haemo
XX Haemo
XX Hoolf
XX 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             문
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                                                                                                                                                                                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
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The specification describes mutant Neutrophil Inhibitory Factors (NIFS), C where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197, 20 or 223 in the wild type sequence (see AAY23591) is replaced by a Gin residue. NIFS may be useful for treating shock, stroke, acute and chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid arthritis, inflammatory skin diseases, inflammatory bouel disease, adult respiratory distress syndrome (ARDS), ischemia-reperfusion injury following myocardial infarction, and acute inflammation caused by acterial infection such as sepsis or bacterial meningitis. NIFS or NIF fragments may be used as vaccines against parasitic worm infection. Anti-NIF antibodies may be useful for detecting infection of a mammalian host by a parasitic worm, as antihelminic agents, and in the detection and isolation of NIF from tissue homogenetes, cloned cells etc. NIFS may be useful for the detection of NIF minics or antagonists in other compounds. Other NIF agonists and inhibitors may also be used as antihelminic agents. AAY23592-98 represent isoform clones of canine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
04-JUL-1996;
                                                     04-JUL-1997;
                                                                                                             15-JAN-1998.
                                                                                                                                                                     WO9801550-A2
                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haemonchus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ES24; antigen; excretory secretory trichostrongylid protein; diarrhoea; anaemia; gastro-intestinal nematode; vaccine; sheep;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haemonchus contortus ES24 antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW37166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW37166 standard; Protein; 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hookworm NIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 10; Fig 9A-E; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inflammatory responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 FGCAVVNCPLGKPDAIITDDEENYATAIHVVCHYPKINKTEGOPIYKVGTPCDDCSEY 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 DENKYIFENSN-NISEAALKAMISWAKEAFNLNKTGEGVLYRSNLTISNFANLAWDTREK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 EENVDVFSAATLNI---PLEAGNSWWSEIFEL----RGKVYNKNGKTSNIANNVWDSHDK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 DDDMREMFTELHNGYRAAFARNY--KTSKMRTMVYDCTLEEKAYKSAEKC---SEEPSSE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 DDD-----YEYGFLPDFAPRASKMRYLEYDCEAEKSAYVSASNCSNISSPPEGY 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                  contortus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                 97WO-NL00380
                                                                                                                                                                                                                       /label=
114..116
/note=
                                                                                                                                                                                                                                                                                                             /label= Sig_peptide
20...222
                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                116
- "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.6%; Score 255; DB 20; 36.5%; Pred. No. 3.3e-18; tive 18; Mismatches 55;
                                                                                                                                                                                                                                                                         Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163
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RESULT 34
AAR26785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This polypeptide comprises the excretory secretory (ES)

trichostrongylid protein ES24 of the gastro-intestinal nematode

Rememonius contortus. Its amino acid sequence was deduced from a

cDNA clone (see AAV03016) isolated from an L5 larval cDNA library.

Also claimed is the a recombinant ES24 polynucleotide comprised in

a vector, and a vaccine for combatting H. contortus infections in

sheep or goats that comprises the recombinant polynucleotide or the

ES24 protein. Vaccines are also provided that contain or express

the ES15 protein (see AAW37165) of H. contortus or the ES14.0 (see

ES24 protein (see AAW37165) antigen of Cooperia oncophora.

Trichostrongylids are a major constraint in ruminant production

world-wide, e.g. producing diarrhoea or anaemia leading to reduced

milk, meat and wool production. To enhance immunogenicity, the ES

coupled with other compounds, e.g. adjuvants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                  Sequence of a homologue of the 45 kD antigen encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR26785;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Page 26; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polynucleotide encoding excretory secretory trichostrongylid proteins - ES15 or ES24 of Haemonchus contortus or ES14.0 or ES14.2 of Cooperia oncophora, useful for vaccines against gastro-intestinal
                             Region
                                                                                                                                                                                                                                                                                                                    PBTA879
                                                                                                                                                                                                                                                                                                                                                                                                             26-JAN-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR26785 standard; Protein; 454 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cornelissen AWCA, Schallig HDFH;
                                                                                                Region
                                                                                                                                                                                             Haemonchus
                                                                                                                                                                                                                                                     Antigen; vaccine; parasitic nematode; immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYUT-) RIJKSUNIV UTRECHT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1998-101048/09.
DB; AAV03016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 GNPCTNNEDCKCTNCVCSRD--EALCI 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 PYDNVMTMAVFNRGVGHYTQVVWQWSNKIGCAVEWCSDMTFVACEYDSAGNYMGMPIYEV 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 VYNK-----NGKTSNIANMVWDSHDKLGCAVVDCSGKTHVVCQYGPEAKGDGKTIYEE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154 GAPCSRCSDYG-AGVTCDDDWQNLLCI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 IEENTMNFAKKCVFAHNSYSESNNWGQNLYMTSILNQNKTVAAAESVDLWFDEL-QQNGV 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 LEEKAYKSAEKC--SEEPSSEEEN--VDVFSAATLN----IPLEAGNSWWSEIFELRGK 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 GHASMCPDTNGMSDEVROTFVNKHNAYRTLVAKGEAKNAKEIGGYAPKAARMLKVTYDCA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GDYSLCQQREKLDDDMREMFTELHNGYRAAFARNY------KTSKMRTMVYDCT 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         222 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                             22..42
/note= "homologous to 45 kD protein"
253..273
                                                                                                Location/Qualifiers
22..42
/note= "see above"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.5%; Score 214; DB 19; Length 222; 28.0%; Pred. No. 6.6e-14; tive 28; Mismatches 89; Indels 32; Gaps
                                                                                            RESULT 35
AAR26786
ID AAR26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCR primers Al12/301 and Al12/302 were designed to be used to campilify the DNA encoding the 45 kD protein. In the reaction containing primer Al12/301 a unique band of approximately 650 bp was containing primer Al12/301 a unique band of approximately 650 bp band was not seen when primer Al12/302 was used. The PCR cloned was grown and purified for use as call 2/302 was used. The PCR cloned was grown and purified for use as a hybridisation probe to screen the pBTA879 cDNA library. pBTA879 cC is the sequence of one of these clones. There is no methionine contain codon present in this region of the sequence so this clone probably does not represent the complete coding region. pBTA879 cC identical to, the native glycoprotein which is related to, but not contain to isolate a cDNA clone coding for the full length native 15 classical to, the native glycoprotein isolated from H. contorcus. The order to isolate a cDNA clone coding for the full length native 15 clones, pBTA879. AAQ28094 is the sequence of one of these clones, pBTA879. AAQ28094 is the sequence of one of these clones, pBTA879. AAQ28094 is the sequence of the contain an contain many contain an experience were screened with the fragment contains and contain many contains and contain many contains and contain and contain many contains and contain many contains and contain many contains and contain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                             AAR26786;
                                                                                         AAR26786 standard; Protein; 440 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vaccines comprise antigens derived from parasitic nematodes - useful for passive immunisation against round, whip, filariasis, thread and hookworms on host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  initiation methionine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 15; Fig 7; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAQ28093.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1992-299990/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cobon GS, Sharp PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BIOT-) BIOTECH AUSTRALIA PTY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-AUG-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9213889-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                 442 CTCSRD--EGLCV 452
                                                                                                                                                                                                                                                                                                            167 VTCDDDWQNLLCI 179
                                                                                                                                                                                                                                                                                                                                                                            382 SKYSQLAWQSSDRIGCVVVPCWSSWTVVVCEYNPGGDLPGEAIYDVGDPCTKDADCQCPG 441
                                                                                                                                                                                                                                                                                                                                                                                                                                       109 SNIANMYWDSHDKLGCAVVDC-SGKTHVVCQYGPEAKGDGKTIYEEGAPCSRCSDYGA-G 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      322 FGLNTAAMLKRWGNNMHMMSSKANNKTEAAAEAVAAWFGDLQKYGVPENNVFTMNVYTTL 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 262 MTDEARKMEYDKHNEYRSLIAKGQAKGKPGQFAPKAARMMKVNYDCDVEANAMEWSKTCT 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 EEPSSEE-----ENVDVFSAATLN---IPLEAGNSWWSEIFEL---RGKVYNKNGKT-- 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 LDDDMREMFTELHNGYRAAFARNY------KTSKMRTMVYDCTLEEKAYKSAEKCS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          454 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91AU-0004486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92WO-AU00040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "homologous with Endoproteinase Lys-C
peptide"
302..0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "as above"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wagland BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 205; DB 13; Length 454; Pred. No. 1.6e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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containing primers Al12/301 and Al12/302 were designed to be used to containing primer Al12/301 and unique band of approximately 550 bp containing primer Al12/301 a unique band of approximately 550 bp band was not seen when primer observed. The approximately 550 bp band was not seen when primer cobserved. The approximately 550 bp band was not seen when primer a hybridisation probe to screen the pBTA879 cDNA library. pBTA879 is the sequence of one of these clones. There is no methionine is the sequence of one of these clones. There is no methionine in that one codon present in this region of the sequence so this clone in tration codon present in this region of the sequence this clone is probably does not represent the complete coding region. pBTA879 comprobed by the patitive glycoprotein which is related to, but not probably encodes a glycoprotein which is related to, but not is clantical to, the native glycoprotein isolated from H. contortus. In order to isolate a cDNA clone coding for the full length native isolated from pBTA879. AAQ28094 is the sequence of one of these clones, pBTA 963. Once again, this clone does not contain an interior methionine.
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Si
Matches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence of a homologue of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JAN-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 рвтА963.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haemonchus contortus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-AUG-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaccines comprise antigens derived from parasitic nematodes useful for passive immunisation against round, whip, filariasis, thread and hookworms on host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cobon GS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BIOT-) BIOTECH AUSTRALIA PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Fig 8; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAQ28094.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       initiation methionine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1992-299990/36.
                                                                             125 GVPDENILTMEVFDRGVGHYTQVAWQSSDKIGCAVEWCPTMTLVACEYNPAGNRINHYIY
                            152
                                                                                                                                                                                                                                                                                                                                                              13 LDDDMREMETELHNGYRAAFARNY------KTSKMRTMYYDCTLEEKAYKSAEKCS 62
                                                                                                                                                                                                                                                       63 EEPSSEEENVDVFSAATLNIPLEAGNSWWSEIFELRGKVYNK--NGKTS-------
                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sharp PJ,
                                                                                                                                  FE-------HDPPEQRNYWGQNLWMLGGTNYSKTESAKLSVQAWYWELKMF
EEGAPCSRCSDYGAGVTCDDDWQNLLCIG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  440 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91AU-0004486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92WO-AU00040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "homologous 239..256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wagland BM;
                                                                                                                                                                                                                                                                                                                                                                                                                              20.2%; Score 201; DB 13; Length 440; 26.8%; Pred. No. 4e-12; tive 23; Mismatches 60; Indels 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "see above"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45 kD antigen encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                õ
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                                                                                                                                                                                                                           124
                                                                                                                                                                                                                                                                                109
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AARS 12990
ID AARS 2990
AC AARS 2
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RESULT 37
AAY23598
ID AAY
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AC AAY
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Best Local S:
Matches 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Canine hookworm Neutrophil Inhibitory Factor isoform 6FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neutrophil inhibitory factor; NIF; glycoprotein; endoparasite; nemattode; parasitic worm; canine hookworm; peritoneal inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-JUN-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A canine hookworm cDNA library was screened with a probe amplified using primers 30.2 and 43.3.RC(AAQ52476 and AAQ52477, respectively) which were based on sequences of isolated NIF peptide fragments. Seven which were based on sequences of isolated for sequence analysis. One of the 120 positive clones were isolated for sequence analysis. One isolate, designated clone IFL, encoded an 825 nucleotide open reading frame (AAQ52475). The other clones contained partial ORFs and encoded partial NIF polypeptides (see AAR52985-R52990) which are thought to represent six NIF isoforms that are significantly similar to, but represent to, the prototypical NIF-IFL polypeptide (AAR42488).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9323063-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ancylostoma caninum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-MAY-1992;
24-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-NOV-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New neutrophil inhibitory factor from parasitic worms - for preventing and treating inflammation, also derived nucleic acid, vectors, transformed hosts and antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1993-386208/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORV-) CORVAS INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 10; Fig 9; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Foster DL, Moyle M, Vlasuk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                               AAY23598 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 185 DIGDPC-----TTDEDWQ---CTG
                                                                                                                                                                                                                                                  100 SERSAYNSASNCSDSSSPPEGYDENKYILENSSNIN---EAARLAIISWGKEAFNLNETG 156
                                                                                                                                                              157
                                                                                                                                                                                                                                                                                                                                                                                    15 DDMREMETELHNGYRAAFARNY------49
                                                                                                                                                                                                     98 RGKVYNKNGKTSNIANMVWDSHDKLGCAVVDC 129
                                                                                                                                                                                                                                                                                           50 LEEKAYKSAEKCSEE---PSSEEENVDVF-SAATLNIPLEAGN----SWWSEIFEL---- 97
                                                                                                                                                                                                                                                                                                                                           40
                                                                                                                                                                                                                                                                                                                                                                                                                                       50;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 32.9%
50; Conservative
                                                                                                                                                                                                                                                                                                                                        DSIRLQFLAMHNGYRSNLALGHIGISKESIGDDYDDDYYYFYSSYAPMASKMRYLEYDCD 99
                                                                                                                                                              EGVLYRSNLTISNFANLAWDTREKFGCAVVKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92US-0881721.
92US-0996972.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93WO-US04502
                                                    Protein; 189
                                                                                                                                                                                                                                                                                                                                                                                                                              20.1%; Score 200; DB 14; Length 189; 32.9%; Pred. No. 1.5e-12; tive. 16; Mismatches 46; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GP;
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                                                                                                                                                                            188
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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157

EGVLYRSNLTISNFANLAWDTREKFGCAVVKC

188

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An the specification describes mutant Neutrophil Inhibitory Factors (NIFs), CC where at least 1 of the Asp residues at positions 18, 87, 110, 130, 137, CC where at least 1 of the Asp residues at positions 18, 87, 110, 130, 137, CC where at least 1 of the Asp residues at positions 18, 87, 110, 130, 137, CC or 223 in the wild type sequence (see AAY23591) is replaced by a Gin CC crimonic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid CC chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid CC captiratory distress syndrome (ARDS), ischemia-reperfusion injury CC respiratory distress syndrome (ARDS), ischemia-reperfusion injury CC complicatory distress syndrome (ARDS), ischemia-reperfusion injury CC following myocardial infarction, and acute inflammation caused by CC compounts may be used as vaccines against parasitic worm infection.

CC fragments may be used as vaccines against parasitic worm infection of a mammalian CC anti-NIF antibodies may be useful for detecting infection of a mammalian CC anti-NIF antibodies may be useful for detecting infection of a mammalian CC and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may CC and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may CC and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may CC and isolation agents. AAY33592-98 represent isoform clones of canine CC compounds. Other NIF agonists and inhibitors may also be used as antihelminic agents. AAY33592-98 represent isoform clones of canine
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neutrophil inhibitory factor; NIF; mutant; shock; stroke; allograft rejection; vasculitis; autoimmune diabetes; ARDS; rheumatoid arthritis; inflammatory skin disease; myocardial infarction; inflammatory bowel disease; adult respiratory distress syndrome; ischemia reperfusion injury; acute inflammation; bacterial infection; vaccine; parasitic worm infection; antihelminic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canine hookworm neutrophil inhibitory factor isoform clone 1P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US5919900-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ancylostoma caninum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-DEC-1993;
11-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mutant Neutrophil Inhibitory Factors useful for treating inflammatory conditions and especially to prevent or decrease inflammatory responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CORV-) CORVAS INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 10; Fig 9A-E; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Foster DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hookworm NIF.
                                                                                       100 SERSAYMSASNCSDSSSPPEGYDENKYILENSSNIN---EAARLAIISWGKEAFNLNETG 156
                                                                                                                                                                                                                                                              50 LEEKAYKSAEKCSEE---PSSEEENVDVF-SAATLNIPLEAGN----SWWSEIFEL----
                                                                                                                                                                                                                40
                              86
                                                                                                                                                                                                                                                                                                                                              50;
                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                DSTRLOFLAMHNGYRSNLALGHIGISKESIGDDYDDDYYYFYSSYAPMASKMRYLEYDCD
RGKVYNKNGKTSNIANMVWDSHDKLGCAVVDC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189 AA;
                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93US-0173510.
92US-0881721.
92US-0996972.
93US-0060433.
93US-0151064.
95US-0450497.
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                                                                                                                                                                                                                                                                                                                                                                                20.1%;
                                                                                                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                                                                                                                                                                                    Score 200;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                          Score 200; DB 20;
pred. No. 1.5e-12;
; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                 46;
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 189;
                                                                                                                                                                                                                                                                                                                                                             indels 40;
                                                                                                                                                                                      97
                                                                                                                                                                                                                                               99
                                                                                                                             RESULT 38
ARE13067
ID ARE13067
ID ARE13067
AC ARE13
AC AR
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The present invention relates to a method for inducing angiogenesis in a ctissue. The method comprising contacting the tissue with Oy-ASP. The Oy-CC tissue. The method comprising contacting the tissue with Oy-ASP. The Oy-CC particularly ischaemia, congenital heart disease, myocardial disease or coclusive disease; more particularly cerebrovascular ischaemia, venocardial invention is also used to treat cancer, disbettle contacts and inflammatory disease. Angiogenesis is also central to a cretinopathy and inflammatory disease. Angiogenesis is also central to a comment of pathological processes, including abnormalities of wound comment of pathological processes, including abnormalities of wound contained in diseases such as diabettes and duodenal ulceration; chronic confinammatory disorders such as rheumatoid arthritis, psoriasis and contact in treat confocerciasis (River Blindness) or benign or malignant consequence is onchocerca volvulus (Oy)-Asp-2 contacts.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anglogenesis; Ov-ASP; therapy; circulatory disorder; vascular disorder; congenital heart disease; myocardial disease; pericardial disease; wart; cerebrovascular ischaemia; veno-occlusive disease, myocardial ischaemia; cerebrovascular ischaemia; retinopathy; inflammatory disease; diabetic retinopathy; inflammatory disease; wound healing; duodenal ulceration; rheumatoid arthritis; psoriasis; wound itis; dermatological; cutaneous malignancy; Kaposi's sarcoma; periodontitis; dermatological; cutaneous malignancy; Kaposi's sarcoma; pyogenic granuloma; cancer; onchocerciasis; River Bindness; neoplasia; vasotropic; cardiant; antiparasitic; opthalmological.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Onchocerca volvulus (Ov)-Asp-2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE13067 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE13067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Onchocerca volvulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200174385-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NYBL-)
(UYCA-)
(UABR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-APR-2000; 2000US-0541759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-MAR-2001; 2001WO-US09798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-662950/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lustigman S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 1; 37pp; English.
                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEW YORK BLOOD CENT INC.
UNIV CASE WESTERN RESERVE.
UAB RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              angiogenesis in a tissue using the Ov-ASP protein isolated nematode Onchocera volvulus is useful to treat circulatory disease such as ischemia
                                                                                          253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pearlman E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Signal_peptide
14..253
/label= Mature_Ov-Asp-2_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
          19.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unnasch TR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253
                    Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₹
                190;
No. 2.
                          DB 22;
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Gaps

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Angiogenesis; Ov-ASP; therapy; circulatory disorder; vascular disorder; congenital heart disease; myocardial disease; pericardial disease; wart; cerebrovascular ischaemia; veno-occlusive disease; myocardial ischaemia; coronary artery disease; diabetic retinopathy; inflammatory disease; wound healing; duodenal ulceration; rheumatoid arthritis; psoriasis; wound healing; dermatological; cutaneous malignancy; Kaposi's sarcoma; pyogenic granuloma; cancer; onchocerciasis; River Blindness; neoplasia; vasctropic; cardiant; antiparasitic; opthalmological.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Onchocerca volvulus (Ov)-Asp-3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE13068;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Onchocerca volvulus.
                                                                                                                                                                                                                                          Inducing from the
                                                                                                                                                                                                                                                                                                                                                                                                                        (NYBL-)
(UYCA-)
(UABR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-APR-2000; 2000US-0541759.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-MAR-2001; 2001WO-US09798
The present invention relates to a method for inducing angiogenesis in tissue. The method comprising contacting the tissue with Ov-ASP. The Ov ASP molecules are used to treat circulatory or vascular disorders, particularly ischaemia, congenital heart disease, myocardial disease or pericardial disease, more particularly cerebrovascular ischaemia, veno-
                                                                                                                                                                Claim 1; Fig 1; 37pp;
                                                                                                                                                                                                                                                                                                                       WPI; 2001-662950/76.
                                                                                                                                                                                                                                                                                                                                                                           Lustigman S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61;
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                                                                                                                                                                                                                                                                                                                                                                                                                        NEW YORK BLOOD CENT INC.
UNIV CASE WESTERN RESERVE.
UAB RES FOUND.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNKYTSIVANRGVSNRTQLAWGKTYKVGCGIATHCDGGKAFVAVCQYNPGGNTMGESIYE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QCVSGNSPKDRRGRIGENVYTQRSDTSVAVYGTSGIMIALE---SWWYEL--TRSYKNNP 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KCSEEPSSEEE-------NVDVFSAATLNIPLEAGNSWWSEIFELRGKYYNK 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KGRPCKTDRDCSSRKCCKRIW 216
                                                                                                                                                                                                                angiogenesis in a tissue using nematode Onchocera volvulus is disease such as ischemia .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 Pearlman E, Unnasch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label- Signal_peptide
17..220
/label- Mature_Ov-Asp-
                                                                                                                                                                   English.
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                                                                                                                                                                                                                                                                                                                                                                                    TR;
                                                                                                                                                                                                                                                 the Ov-ASP protein isolated useful to treat circulatory
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AAE
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Matches 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Angiogenesis; Ov-ASP; therapy; circulatory disorder; vascular disorder; congenital heart disease; myocardal disease; pericardial disease; wart; cerebrovascular ischaemia; veno-occlusive disease; myocardal ischaemia; coronary artery disease; diabetic retinopathy; inflammatory disease; wound healing; duodenal ulceration; rheumatoid arthritis; psoriasis; periodontitis; dermatological; cutaneous malignancy; kaposi's sarcoma; psogenic granuloma; cancer; onchocerciasis; River Blindness; neoplasia; vascuropic; cardiant; antiparasitic; opthalmological.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Onchocerca volvulus (Ov)-Asp-1 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Key
Peptide
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                                (NYBL-)
(UYCA-)
(UABR-)
                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                       03-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 Similarity 27.9
55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REKLDDDMREMETELHNGYRAAFAR-NY------KTSKMRTMVYDCTLEEKAYKSAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KC--SEEPSSEEE------NVDVFSAATLNIPLEAGNSWWSEIFELRGKVYNK 104
                                NEW YORK BLOOD CENT INC.
UNIV CASE WESTERN RESERVE.
UAB RES FOUND.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGAPC----SRCS 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               volvulus.
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                                                                                                                                                                                                                                                                                                                                                    /label= Signal_peptide
14.223
/label= Mature_Ov-Asp-1_protein
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Pred. No. 4.2e-11;
9; Mismatches 63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 220;
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RESULT 31

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RESULT 41
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Best Local
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Human; FCTRX; myelogenous leukaemia; carcinoma; melanoma; glioma; astrocytoma; congenital neonatal alloimmune thrombocytopaenia; infection; neurological disorder; neurological disorder; neurological disorder; neurological disorder; neurodegenerative disorders; nerve trauma; familial myelodysplastic syndrome; Charcot-Marie-Tooth neuropathy; demyelinating Gardner syndrome; familial myelodysplastic syndrome; mental health condition; immunological disorder; allergy; infertility; bronchial asthma; Aveilino type eosinophilia; lung disease; deafness; reproductive disorder; reproductive disorder; reproductive disorder; garcotein in deficiency; desmoid disease; turcot syndrome; liver cirrhosis; hepatitis C; virucide; gastric disorders; pancreatic disease; Schistosoma mansoni infection; spinocerebellar ataxia; plassmodium faiciparum parasitemia; diabetes; corneal dystrophy-Greonouw type I; Corneal dystrophy-lattice type I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human FCTR7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU08687 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein; 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 161.5;
; Pred. No. 1.96
28; Mismatches
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73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22; Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                õ
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                                                                                                                                                                                                                                                                                      The invention relates to human FCTRX polypeptides, FCTR1-FCTR7, and the CC nucled acids encoding them. These sequences are useful for the treatment CC or prevention of numerous disorders including myelogenous leukaemia, C carcinomas, melanomas, gliomas, astrocytomas, congenital neonatal alloimnune thrombocytopaenia, neurological disorders, neurodegenerative CC clarcot-Marie-Tooth neuropathy, demyelodysplastic syndrome, familial myelodysplastic syndrome, familial cc myelodysplastic syndrome, mental health conditions, immunological conventysplastic syndrome, mental health conditions, immunological consinophilia, lung diseases, reproductive disorders, infertility, male cosinophilia, lung diseases, reproductive disorders, infertility, male cosinophilia, lung diseases, reproductive disorders, inspatitis C, gastric consolid disease, turcot syndrome, liver cirrhosis, hepatitis C, gastric cdisorders, pancreatic diseases such as diabetes, schistosoma mansoni confection Spinocerabellar ataxia, Plasmodium faiciparum parasitaemia, corneal dystrophy Greonouw type I, Corneal dystrophy-lattice type I and corneal dystrophy Greonouw type I, Corneal dystrophy corneal dystrophy. This sequence represents FCTR7, a trypsin inhibitor-like protein.
                                                                                                                                                                                    Query Match
Best Local S
Matches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-MAR-2000; 2000US-186592P.
03-MAR-2000; 2000US-18731BP.
06-MAR-2000; 2000US-187293P.
06-MAR-2000; 2000US-187294P.
17-MAR-2000; 2000US-190400P.
07-PAR-2000; 2000US-19041BP.
03-JAN-2001; 2001US-259548P.
                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             states
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polypeptides designated as FCTRX detection, prevention and treatment of states -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-596837/67.
N-PSDB; AAS14095.
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Macdougall J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-MAR-2001; 2001WO-US07160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200166747-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens.
                                                                                                             43
                                                                                                                                                                                    Similarity
53; Conser
                                   RAESCLWEHGPAS-----LLPSIGQNLGAHWGRYRPPTFHVQSWYDEVKDFSYPYEHEC
                                                                       SAEKCSEE--PSSEEENVDVFSAATLNIPLEAG-----NSWWSEI-----
                                                                                                                                     EGDYSLCQQREK---LDDDMREMFTELHNGYRAAFARNYKT-SKMRTMVYDCTLEEKAYK 56
----FELRGKYYNKNGKTSNIANMVWDSHDKLGCAVVDCSG
                                                                                                             DGEWWIAKQRGKRAITDNDMQSIL-DLHNKLR----SQVYPTASNMEYMTWDVELERSAES
                                                                                                                                                                                                                                                              300
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J, Mishra V
                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215pp; English.
                                                                                                                                                                                                    16.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shimkets RA, Herrmann JL, Mezes PS, Rastelli L;
                                                                                                                                                                                    Score 160; DB 22;
Pred. No. 4.2e-08;
31; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptides,
a broad range
                                                                                                                                                                                                                        Length 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful in of pathological
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RESULT AND SULT OF SUL
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
                                                                                   The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cencer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and c N & Misorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 200
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tang
Wang
                    assays for receptor activity, arthritis and C.N.S disorders.
Note: The sequence data for this patent did specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              such
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; SEQ ID NO 2861; 10078pp; English.
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DB; AAI58872.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acids and polypeptides, useful as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang z,
zhou P,
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2000US-052317.
2000US-0598042.
2000US-0520312.
2000US-0620312.
2000US-0662191.
2000US-0593036.
2000US-0727344.
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Wehrman T, X:
~~drich R,
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, Xu C, Xue
R, Drmanac R
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еал,
RT;
                                            not form part of the printed
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Yang Y,
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Zhang
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Best Local
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                                                                                                                                                                                  21-JAN-2000; 2000US-0488725.

25-APR-2000; 2000US-0552317.

09-JUL-2000; 2000US-0598042.

19-JUL-2000; 2000US-062031.

03-AUG-2000; 2000US-0623450.

14-SEP-2000; 2000US-0663191.

19-OCT-2000; 2000US-0663191.

29-NOV-2000; 2000US-0727344.
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the
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Wang
2hao
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N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                  Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; SNy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                 Example 2; SEQ ID NO 6433; 10078pp; English.
                                                    Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
                                                                                                                                                                                                                                                                                     26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                                                                WO200153312-A1.
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                                                                                                                                                                                                                                                                                                                                                                          leukaemia.
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invention relates to encoded polypeptides
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                                                                                     2001-442253/47.
)B; AAI60658.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86 GENLFAITDEGMDVPL-AMEEWHHE-----REHYNLSAATCSPGQMCGHYTQVVWAKTER
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                                                                                                                    , Liu C,
Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KNSLC 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QNLLC 178
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Wehrman T, 2
, Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein; 347
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 human nucleic acids (AAM38642-AAM42213)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    6433.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 159; DE
Pred. No. 4.5e
%6; Mismatches
                                                                                                                     Chen R, Ma Y,
Xu C, Xue AJ,
R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22;
.5e-08;
les 72;
                                                                                                                              Qian >
 (AAI57798-AAI61369) and with nootropic,
                                                                 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 266;
                                                                treating
                                                                                                                               g xB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                               Ren F, 1
Zhang J;
                                                                disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34;
                                                                                                                                          Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173
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RESULT 44
AAY13392
ID AAY13
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Best Local S
Matches 53
                          25-NOV-1997;
17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Secreted protein; transmembrane protein; human; enterocolitis; Sollinger-Ellison syndrome; gastrointestinal ulceration; congenital microvillus atrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin; dermal scarring; Ubber Syndrome; Atrophia areata; anti-thrombotic; wound healing; tissue repair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polyneptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as alzheimer's, parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer disgnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and c.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY13392 standard; Protein; 463 AA.
         18-SEP-1997;
                                                                                                                                                                                                                                                                                                                                          25-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                            WO9914328-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of protein PRO328.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY13392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                      16-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270 KNSLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174 QNLLC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGCAVVDCS-----GKTHV----VCQYGPEAKGDGKTIYEEGAPCSRCSDYGAGVTCDDDW 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENLFAITDEGMDVPL-AMEEWHHE-----REHYNLSAATCSPGQMCGHYTQVVWAKTER 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EENVDVFSAATLNIPLEAGNSWWSEIFELRGKVYNKNGKTSNIANM------VWDSHDK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTDEEKRLMVELHNLYRAQVSPT--ASDMLHMRWDEELAAFAKAYARQCVWGHNKERGRR 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQCP---SGYHC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             347 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
970S-0066840
970S-0059113
970S-0059115
970S-0059117
970S-0059117
970S-0059121
970S-0059121
970S-0059184
970S-0059184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 34;
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18-SEP-1997;
15-OCT-1997;
17-OCT-1997;
                                                                                        (GETH ) GENENTECH INC.
                                                                                                                                                 9705-0063128

9705-0063327

9705-0063341

9705-0063541

9705-0063344

9705-0063344

9705-006356

9705-006356

9705-006356

9705-0063732

9705-0063732
                                                                                                                                                                                                            970S-0059266.
970S-0062125.
970S-0062285.
                                                                                              970S-0066453
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Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan Ç,

WPI; 1999-229533/19. N-PSDB; AAX52263.

New isolated human genes and polypeptides used in, gastrointestinal ulceration e.g. treatment of

Claim 12; Fig 100; 320pp; English.

CC AAX13344-403 represent secreted and transmembrane human proteins.
CC The cDNA sequences are obtained from cDNA libraries, prepared from
CC fetal lung, fetal kidney, fetal brain, fetal livrar and fetal retina.
CC The encoded polypeptides have specific uses based on their homology to
CC known polypeptides, e.g. PRO211 and PRO217 can be used for disorders
CC associated with the preservation and maintenance of gastrointestinal
CC mucosa and the repair of acute and chronic mucosal lesions
CC (e.g. enterocolitis, Zollinger-Fillison syndrome, gastrointestinal
CC ulceration and congenital microvillus atrophy), skin diseases associated
CC with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial
CC cancers such as lung squamous cell carcinoma of the vulva and gilomas),
CC potent effects on cell growth and development, diseases related to
CC growth or survival of nerve cells including Parkinson's disease,
CC for fibromodulin, e.g. for reducing dermal scarring. PRO265 can be used
CC as a target for anti-tumor drugs. PRO333 may be used in the treatment
CC anti-thrombotic agent, PRO287 polypeptides and portions may have
CC therapeutic applications in wound healing and tissue repair; PRO317 can

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RESULT 45
AABOLT 47
AABOLT 47
AABOLT 47
AABOLT 47
AABOLT 47
AABOLT 47
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AAABOLT
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Best Local S
Matches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neuron associated protein; NEUAP; neurological disorder; epilepsy; ischemic cerebrovascular disease; stroke; cerebral neoplasm; Alzhelmer; disease; pick; disease; stroke; cerebral neoplasm; Alzhelmer; disease; pick; disease; dementia; parkinson; disease; demyelinating disease; meningitis; prion disease; neuro; creutzfeldt-Jakob disease; neurofibromatosis; cerebral palsy; muscular dystrophy; central nervous system; cNS; peripheral nervous system; PNS; myopathy; schizophrenia; actinic keratosis; arteriosclerosis; atherosclerosis; bursitis; arteriosclerosis; atherosclerosis; bursitis; myopathy; schizophrenia; nyolofibrosis; paroxysmal nocturnal haemoglobinuria; cancer; autoimmune disease; inflammation; acquired immunodeficiency syndrome; allergy; ankylosing spondylitis; amyloidosis; anaemia; asthma; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         be used vessels,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Peptide
                                                                                             Disulfide-bond
                                                                                                                                           Disulfide-bond
                                                                                                                                                                                                                                         Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
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                                                Modified-site
                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neuron-associated protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity 28.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KNSLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QNLLC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENLFAITDEGMDVPL-AMEEWHHE-----REHYNLSAATCSPGQMCGHYTQVVWAKTER 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQCP---SGYHC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EENVDVFSAATLNIPLEAGNSWWSEIFELRGKVYNKNGKTSNIANM-----VWDSHDK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTDEEKRLMVELHNLYRAQVSPT--ASDMLHMRWDEELAAFAKAYARQCVWGHNKERGRR 85
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                                             /note-
126
/note-
137
                                                                                                                                                                                           /note=
114
                                                                                                                                                                                                                                                                                      /note-
                                                                                                                                                                                                                                                                                                                                       /note-
29
                                                                                                                                              /note-
120
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                  'note-
                                                                                                                                                                                                                                                                                                                                                                                                        /label= Signal peptide
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                      "Potential phosphorylation site"
                                                                       *Potential
                                                                                                                    "Potential
                                                                                                                                                                                                               "Potential disulfide bond forming
                                                                                                                                                                                                                                                                "Potential
                                                                                                                                                                                                                                                                                                       "Potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                        "Potential disulfide bond forming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26;
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Pred. No. 9.8e
26; Mismatches
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in the heart of genital tract.
                                                                                                                                                                                                                                                             phosphorylation site"
                                                                 disulfide bond forming
                                                                                                                 disulfide bond forming
                                                                                                                                                               glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 20;
.8e-08;
es 72;
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                                                                       residue"
                                                                                                                    residue"
                                                                                                                                                                                                                  residue"
                                                                                                                                                                                                                                                                                                                                                              residue"
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11-DEC-1998;
11-DEC-1998;
09-FEB-1999;
16-MAR-1999;
                                                                                     Tang YT,
New human neuron-associated proteins and polynucleotides encoding thuseful for diagnosis, treatment and prevention of cell proliferative disorders including cancer, neuronal and neurological disorders
                                                   WPI; 2000-423423/36.
N-PSDB; AAA47414.
                                                                                                                                                                                                                                                                                                                                                                                                             Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disulfide-bond
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                                                                                                                         (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                          10-DEC-1999;
                                                                                                                                                                                                                                 15-JUN-2000.
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                                                                                              TY,
                                                                                    , Yue H, Baughn MR, Azimzai Y;
                                                                                                                                              98US-0210083.
98US-9123456.
99US-0119365.
99US-0124687.
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197
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186
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192
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323
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163
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409
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299
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283
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227
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218
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202
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195
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156
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147
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Claim 1; Page 94-95; 145pp; English.

Human neuron-associated proteins (NEUAP) can be used for for treating or preventing a disorder associated with decreased expression or activity of NEUAP. Antagonists of NEUAP are useful for treating or preventing disorder associated with increased expression or activity of NEUAP. NEUAP or their fragments or derivatives are useful for treating neurological disorder such as epilepsy, ischemic cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease, dementia and parkinson's disease. NEUAPs are also useful for treating other demyelinating diseases, bacterial and viral meningitis, prioniseases including kuru, Creutzfeldt-Jakob disease, nutritional and metabolic diseases of the nervous system, neurosis, other developmental disorders of the central nervous system desorders, other developmental disorders, autonomic nervous system disorders,

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Search completed: July 15, 2003, 08:36:12
Job time: 73 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 15.9%; Score 159; DB 21; Length 463; Best Local Similarity 28.6%; Pred. No. 9.8e-08; Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence . 463 AA;
                                                                                                                                                                               193 KNSLC ·197
                                                                                                                        174 QNLLC 178
                                                                                                                                                                                                                                                                                                     69 EENVDVFSAATLNIPLEAGNSWWSEIFELRGKVYNKNGKTSNIANM------VWDSHDK 121
                                                                                                                                                                                                                                                                                                                                                               28 LTDEEKRLMVELHNLYRAQVSPT--ASDMLHMRWDEELAAFAKAYARQCVWGHNKERGRR 85
                                                                                                                                                                                                                                                                                                                                                                                                           13 LDDDMREMFTELHNGYRAAFARNYKTSKMRTMYYDCTLEEKAYKSAEKC----SEEPSSE 68
                                                                                                                                                                                                                                                                       86 GENLFAITDEGMDVPL-AMEEWHHE-----REHYNLSAATCSPGOMCGHYTQVVWAKTER 139
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Title: Perfect score: Sequence:

US-09-937-555A-2 997 1 EGDYSLCOOREKING

Run on: OM protein

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

sequence

1, Appli
86, Appl
88, Appl
5, Appli
5, Appli
2, Appli
12, Appli
112, Appli
4, Appli
4, Appli
3, Appli
3, Appli
3, Appli

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2003 Compugen Ltd
US-08-173-510B-86
US-08-450-497-86
US-08-450-97-86
US-08-450-97-87
US-08-450-97-930-686-12
US-08-450-98-10
US-08-450-998-10
US-08-450-998-10
US-08-450-998-10
US-08-450-998-10
US-08-450-998-10
US-08-450-998-12
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82, Appli
83, Appli
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85, Appli
10, Appli
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12, Appli
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MEDLUM TYPE: 3.5° Diskette, 1.44 M
MEDLUM TYPE: 8 FORAGE
COMPUTER: EFORAGE
COMPUTER: IBM COMPAtible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: World Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/151,064
FILING DATE: 23-DEC-1993
PRIOR APPLICATION NUMBER: 08/060,433
APPLICATION NUMBER: 08/060,433
APPLICATION NUMBER: 07/996,972
FILING DATE: 11-MAY-1993
APPLICATION NUMBER: 07/996,972
FILING DATE: 11-MAY-1992
APPLICATION NUMBER: 07/981,721
FILING DATE: 11-MAY-1992
APPLICATION NUMBER: 07/881,721
FILING DATE: 11-MAY-1992
APPLICATION NUMBER: 30,18
REFERENCE/DOCKET NUMBER: 30,18
REFERENCE/DOCKET NUMBER: 205/073
TELECOMMUNICATION INFORMATION:
TELEPHAN: (213) 489-1600
TELES: 67/3510
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 ANINO ACIDS
TYPE: AMINO ACIDS
TYPE: AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 1
US-08-173-510B-86
                MOLECULE TYPE: -08-173-5108-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MATTHEW MOYLE, TITLE OF INVENTION: NOVEL NUMBER OF SEQUENCES: 104 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Lyon & I
STREET: 633 West F1
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                  LENGTH: 231 AMINO ACIDS TYPE: AMINO ACID TOPOLOGY: LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U
ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NO. 5/4/-
AL INFORMATION:
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633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U.S.A.
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NEUTROPHIL INHIBITORS
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US-08-173-510B-88
US-08-458-218-86
US-08-450-944-7-88
US-08-450-944-5
PCT-US96-07709-5
US-08-450-944-5
US-08-450-949-8
US-08-773-368-4
US-09-199-887-3
US-09-7199-887-3
US-09-7199-887-3
US-09-7199-887-3
US-09-1199-887-3
US-09-1199-887-3
US-09-1199-887-3
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US-09-1199-887-3
US-09-1199-887-3
US-09-1199-887-3
US-09-1199-87-248-111
US-09-1199-87-248-111
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US-09-1199-87-3
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Result No.

Score

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290.5 290.5 290.5 290.5 290.0 290.0 290.0 290.0 290.0 290.0 290.0 290.0 290.0 205.5 255.5 255.5 255.0 205.0 200.0

Query Match

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191 137

ent No.

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RESULT 2
US-08-458-218-84
                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION UNDER: 30,158
REFERENCE/DOCKET NUMBER: 203/
TELECOMMUSICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                          TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/151,064
FILING DATE: 10-NOVEMBER: 1993
APPLICATION NUMBER: 08/060,433
FILING DATE: 11-MAY-1993
APPLICATION NUMBER: 07/981,721
FILING DATE: 11-MAY-1992
APPLICATION NUMBER: 07/996,972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDA...
STREET: ...
STREET: Suite ...
CITY: Los Angeles
CITY: California
U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Word Perfec-
CURRENT APPLICATION DATA
APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM CO
OPERATING SYSTEM:
                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37 KTSKMRTMVYDCTLEEKAYKSAEKCSEEPSSE------EENVDVFSAATLNIPLEA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 ICSONGTGMFGFNDSMRLKFLEMHNGYRSRLALGHISITEEPESYDDDDDYGYSEVLYAP 75
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74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4, Application US/08458218
5789178
                                                                                        AMINO ACID
                                                          TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHY-PKIEGEEKEGKQIYKVGTPCGDCSEY 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CQYGPEAKG---DGKTIYEEGAPCSRCSDY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -LSWAKEAFDLNKTGEGVLYRSNLTISNFANLAWDTREKFGCAVAKCPLKDTSATTIHVV 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNSWWSEIFEL----RGKVYNKNGKTSNIANMVWDSHDKLGCAVVDCSGK-----THVV 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SASKMRYMEYDCEAEKSAYKSASSCSDSSSSSPEGYDENKYILENSSNISEAARLAI---- 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MATTHEW MOYLE ET AL.

ENTION: NOVEL NEUTROPHIL INHIBITORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Word Perfect 5.1
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  30.0%;
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  Score
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  299;
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Length 231;
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                                    ; MOLECULE TYPE: US-08-450-497-86
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US-08-450-497-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 35. Matches 74; Conservative
Query Match
                                                                                        TELERAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 AMINO ACIDS
TYPE: AMINO ACIDS
TYPE: AMINO ACIDS
                                                                                                                                                                                                                                                          PILING DATE:
PRIOR APPLICATION DATA:
APPLICATION UNBER: 08/173,510
FILING DATE: 23-DEC-193
APPLICATION NUMBER: 08/151,064
FILING DATE: 10-NOV-1993
APPLICATION NUMBER: 08/060,433
FILING DATE: 11-MAY-1993
APPLICATION NUMBER: 07/996,972
FILING DATE: 24-DEC-1992
APPLICATION NUMBER: 07/881,721
FILING DATE: 11-MAY-1992
APPLICATION NUMBER: 07/881,721
FILING DATE: 11-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REGISTRATION NUMBER: 30,158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C.
SOSTWARE: WORD PRIECT 5.1
CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5° DI
MEDIUM TYPE: storage
                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 20:
                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Los Angeles
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132. -LSWAKEAFDLNKTGEGVLYRSNLTISNFANLAWDTREKFGCAVAKCPLKDTSATTIHVV 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87 GNSWWSEIFEL----RGKYYNKNGKTSNIANMYWDSHDKLGCAVVDCSGK-----THVV 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 SASKMRYMEYDCEAEKSAYKSASSCSDSSSSPEGYDENKYILENSSNISEAARLAI---- 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 KTSKMRTMVYDCTLEEKAYKSAEKCSEEPSSE------EENVDVFSAATLNIPLEA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 ICSQNGTGMFGFNDSMRLKFLEMHNGYRSRLALGHISITEEPESYDDDDDYGYSEVLYAP 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CQYGPEAKG---DGKTIYEEGAPCSRCSDY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Lyon & Lyon
633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08450497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MATTHEW MOYLE, ET AL. JENTION: NOVEL NEUTROPHIL INHIBITORS
                                                          PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.2%; F-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diskette, 1.44 Mb
  30.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/08/450,497
                                                                                                                                                                                                                                          205/073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 4.2e-25;
0; Mismatches 58;
  Score 299;
  DB
  27.
  Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58;
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Query Match

RESULT 4 US-08-173-510B-84

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191

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87

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COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM COMPATIBLE
ODERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WOO'D PATE: 5.1
CURRENT APPLICATION DATA:
APPLICATION DATE: 23 DEC-1993
                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 205/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 35.2%; Pred. No. 4.2e-25; Matches 74; Conservative 20; Mismatches 58;
                                                                                                                                                                                 TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEG ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/151,064
FILING DATE: 10-NOV-1993
APPLICATION NUMBER: 08/060,433
FILING DATE: 11-MAY-1993
APPLICATION NUMBER: 07/996,972
FILING DATE: 24-DEC-1992
APPLICATION NUMBER: 07/881,721
APPLICATION NUMBER: 07/881,721
APPLICATION NUMBER: 07/881,721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MATTHEW MOYLE, ET AL.
TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS
NUMBER OF SEQUENCES: 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los brown
  Match 29.1%; Score 290.5; DB 1; Local Similarity 37.3%; Pred. No. 3.6e-24; es 75; Conservative 23; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84, Application US/08173510B
>. 5747296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 ICSQNGTGMFGFNDSMRLKFLEMHNGYRSRLALGHISITEEPESYDDDDDYGYSEVLYAP 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 LCQQREK----LDDDMREMFTELHNGYRAAFARNY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GNSWWSEIFEL----RKVYNKNGKTSNIANWYWDSHDKLGCAVVDCSGK-----THVV 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -LSWAKEAFDLNKTGEGVLYRSNLTISNFANLAWDTREKFGCAVAKCPLKDTSATTIHVV 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SASKMRYMEYDCEAEKSAYKSASSCSDSSSSPEGYDENKYILENSSNISEAARLAI---- 131
                                           DB 1;
                                             Length 232;
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
  43;
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  Gaps
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  7;
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                                                                                                              ; MOLECULE TYPE: US-08-458-218-82
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US-08-458-218-82
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                                                                                                                                                    TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8
Patent No.
                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/151,064
FILING DATE: 10-NOVEMBER:1993
APPLICATION NUMBER: 08/060,433
FILING DATE: 11-MAY-1993
APPLICATION NUMBER: 07/881,721
APPLICATION NUMBER: 07/881,721
FILING DATE: 11-MAY-1992
APPLICATION NUMBER: 07/996,972
APPLICATION NUMBER: 07/996,972
APPLICATION NUMBER: 07.992
ATTORNEY/ACRUT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,188
REFERENCE FORCE: 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPOTER: IBM COMPATIBLE
OPERATING SYSTEM:
SOFTWARE: WORD Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MATTHEW MOYLE ET ALTITLE OF INVENTION: NOVEL NEUTR
NUMBER OF SEQUENCES: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212 SRRKENPIYTTGNRCGGCSDY 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 AKGDGKTIYEEGAPCSRCSDY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152 ISWATEAFNLNKTGEGVVYRSILDISNFANLAWDTREKVGCAVVKCSPRTTHVVCHYPKK 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82, Application US/08458218
5, 5789178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88 NSWWSEIFEL----RGKVYNKNGKTSNIANWVWDSHDKLGCAVVDCSGK-THVVCQYGPE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 TSKMRTMVYDCTLEEKAYKSAEKCSEEPSSEE---ENV------DVFSAATLNIPLEAG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37
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                  75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EHDPTCPQNGEKMEKGFDDAIRLKFLAMHNGYRSRLALGHVSITEESEDYDLYDLLYAPR 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGDYSLCQQREKL----DDDMREMFTELHNGYRAAFARNY------K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U.S.A.
                29.1%; Score 290.5; DB 1; 37.3%; Pred. No. 3.6e-24; tive 23; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOVEL NEUTROPHIL INHIBITORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/458,218
                                                                                                                                                                                                                                                                                                                                                           203/226
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                Indels 43;
                                                           Length 232;
                Gaps
                7;
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U.S.A.

TYPE: AMINO
TOPOLOGY: L:
MOLECULE TYPE:
US-08-173-510B-84

H: 232 AMINO ACIDS
AMINO ACID
DGY: LINEAR

Best Lo

Query Match 29.1%; Score 290.5; DB 2; Length 232; Best Local Similarity 37.3%; Pred. No. 3.6e-24; Matches 75; Conservative 23; Mismatches 60; Indels 43; Gaps 7;	RESULT 6 US-08-430-494 US-08-430-497-64 Sequence 84, Application US/08450497 Patent No. 5919900 GENERAL IMPORMATION: MOVEL, ET AL. APPLICANT: MATTHEW MOVIE, ET AL. MUNDER OF SEQUENCES: 104 CORRESPONDENCE ADDRESS: LYON 6 LYON STREET: 631 West Fifth Street STREET: 631 West Fifth Street STREET: SAILE 4700 CITY: LOS Angeles GAMPE: CALIFORNIA INFORMATING STREET: 15 "Diskette, 1.44 Mb MEDIUM TYPE: STOUGH, 14 "Mb MEDIUM TYPE: STOUGH, 15 "DISKET SAILE COMPUTER ELDABLE FORM: MEDIUM TYPE: STOUGH, 15 "DISKET SAILE COMPUTER STREET: HAVE OBDATE: COMPUTER STREET: HAVE OBDATE: MEDIUM TYPE: STOUGH, 15 "DISKET SAILE COMPUTER: LAN COMPATINA MEDIUM TYPE: STOUGH, 15 "DISKET SAILE COMPUTER: SAILE COMPUTER: STOUGH, 15 "DISKET SAILE COMPUTER: S	QY 143 AKGDGKTIYEEGAPCSRCSDY 163 ::	Qy 88 NSWMSEIFELRGKVYNKNGKTSNIANMVWDSHDKLGCAVVDCSGK-THVVCQYGPE 142	Qy 1 EGDYSLCQOREKLDDDMREMFTELHNGYRAAFARNY
Similarity 34.3%, Pred. No. 5.3e-24; 9; Conservative 23; Mismatches 57; DDDMEMTTELHNGYRAAFARNY	RESULT 7 108-173-108-83 Sequence 83, Application US/08173510B Sequence 83, Application US/08173510B Sequence 83, Application US/08173510B Patent No 7547956 GENERAL INFORMATION: APPLICANT: MATTHEW MOVIE, ET AL. TITLE OF INVENTION: MOVEL NEUTROPHIL INHIBITORS NUMBER OF SEQUENCES: 104 CORRESPONDENCE ADDRESS: ADDRESSEE: LYON 6 LYON STREET: 531 West Fifth Street STREET: 532 West Fifth Street STREET: 534 West Fifth Street STREET: 535 West Fifth Street STREET: 534 West Fifth Street STREET	QY 143 AKGDGKTIYEEGAPCSRCSDY 163 ::	Qy 88 NSWWSEIFELRGKYYNKNGKTSNIANMYWDSHDKLGCAVYDCSGK-THVYCQYGPE 142	QY 1 EGDYSLCOOREKLDDMRENFTELHNGYRAAFARNY



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RESULT 8 US-08-458-218-81

ENERAL INFORMATION

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U.S.A.

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LENGTH: 274 AMINO ACID
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
US-08-458-218-81
                                                                                                                                                                                                                     TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SED ID NO: 81
SEQUENCE CHARACTERISTICS:
LENGTH: 274 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY:
                                                                        Query Match
Best Local Similarity 34.3
Matches 69; Conservative
                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/151,064

FILING DATE: 10.NOVEMBER: 1993

APPLICATION NUMBER: 08/060,433

FILING DATE: 11.MAY-1993

APPLICATION NUMBER: 07/881,721

FILING DATE: 11.MAY-1992

APPLICATION NUMBER: 07/96,572

FILING DATE: 24-DEC-1992

APPLICATION NUMBER: 07/96,572

APPLICATION NUMBER: 07/96,572

APPLICATION NUMBER: 03/26,572

APPLICATION NUMBER: 20/20,000

REGISTRATION NUMBER: 20/226

TELECOMMUNICATION NIFORMATION:

TELEPINE: (213) 489-1600

TELEPINE: (213) 489-1600

TELEPINE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
SOFTWARE: WORD PARFACT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/4
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214 NKTEGQPIYKVGTPCDDCSEY 234
                                             14 DDDMREMFTELHNGYRAAFARNY--------KTSKMRTMVYDCTL 50
     NDSIRLQFLAMHNGYRSKLALGHISITEESESDDDDDFGFLPDFAPRASKMRYLEYDCEA 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AKGDGKTIYEEGAPCSRCSDY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVLYRSNHDISNFANLAWDAREKFGCAVVNCPLGEIDDETNHDGETYATTIHVVCHYPKI 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKYYNKNGKTSNIANMYWDSHDKLGCAVVDC------SGKT-----SGKT-----HVVCQYGPE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EEKAYKSAEKCSEE---PSSEEENVDVFSAATLNI---PLEAGNSWWSEIFEL-----R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKSAYMSARNCSDSSSPPEGYDENKYIFENSN-NISEAALKAMISWAKEAFNLNKTKEGE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NDSIRLQFLAMHNGYRSKLALGHISITEESESDDDDDFGFLPDFAPRASKMRYLEYDCEA 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/08458218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MATTHEW MOYLE ET AL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM Compatible
                                                                                            29.1%; Score 290; DB 1; 34.3%; Pred. No. 5.3e-24; ative 23; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOVEL NEUTROPHIL INHIBITORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/458,218
                                                                                                                                                                                                                                                                                                          81:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM P.C. DOS 5.0
                                                                                                                                Length 274;
                                                                                          Indels 52;
                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98
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                                                                                       Matches
                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                  TELERAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGRH: 274 MAINO ACIDS
TYPE: AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/173,510
APPLICATION NUMBER: 08/151,064
APPLICATION NUMBER: 08/151,064
APPLICATION NUMBER: 08/160,433
APPLICATION NUMBER: 07/96,972
APPLICATION NUMBER: 07/96,972
APPLICATION NUMBER: 07/981,721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ETLING DATE:
ETLING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/173,510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,497
                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Lyon & Lyon
STREET: 533 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                     Local Similarity
es 69; Conserv
                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 AKGDGKTIYEEGAPCSRCSDY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214 NKTEGOPIYKVGTPCDDCSEY 234
       35
                                        14 DDDMREMFTELHNGYRAAFARNY--------KTSKMRTMVYDCTL 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 EKSAYMSARNCSDSSSPPEGYDENKYIFENSN-NISEAALKAMISWAKEAFNLNKTKEGE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 EEKAYKSAEKCSEE---PSSEEENVDVFSAATLNI---PLEAGNSWWSEIFEL------R 98
NDSIRLQFLAMHNGYRSKLALGHISITEESESDDDDDFGFLPDFAPRASKMRYLEYDCEA 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08450497
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                                                                                     Conservative
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PENTION: NOVEL NEUTROPHIL INHIBITORS
                                                                                                                                                                                              PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                           SUZANNE
                                                                                  29.1%; Score 290; DB 2; Length 274; 34.3%; Pred. No. 5.3e-24; Live 23; Mismatches 57; Indels !
                                                                                                                                                                                                                                                                                                                                                                                             30,158
205/073
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35

Gaps

nes 66; Conservative 21; Mismatches 14 DDDMREMFTELHNGYRAAFARNY 1 :	LENGTH: 224 AMINO ACIDS TYPE: AMINO ACIDS TOPOLOGY: LINEAR MOLECULE TYPE: PEPTIDE US-08-173-510B-87 Query Match Best Local Similarity 33.8%: Pred No. 1 8e-21:	AGENT I BIGGS, WATION N NCE/DOCK JNICATIO SURE: (2 SURE:	APPLICATION NUMBER: US/O8/173,510B FILING DATE: 23-DEC-1993 PRIOR APPLICATION NUMBER: 08/151,064 FILING DATE: 10-NOV-1993 APPLICATION NUMBER: 08/060,433 FILING DATE: 11-NAX-1993 FILING DATE: 11-NAX-1993 FILING DATE: 24-DEC-1992 FILING DATE: 24-DEC-1992 FILING DATE: 34-DEC-1992 FILING DATE: 1-NAX-1993 FILING DATE: 11-NAX-1993 FILING DATE: 11-NAX-1993	1, S	RESULT 10 US-08-173-510B-87 ; Sequence 87, Application US/08173510B ; Patent No. 5747296 ; GENERAL INFORMATION: ; APPLICANT: MATTHEW MOYLE, ET AL. ; TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS ; NUMBER OF SEQUENCES: 104 ; CORRESPONDENCE ADDRESS: ; ADDRESSEE: LVON	Oy 51 EERAYKSAEKCSEEPSSEEENVDVFSAATLNIPLEAGNSWWSEIFELR 98 :
14 DDDMRHTELHNGYRAFARNY	AMING ACID AMING ACID Y: LINEAR Y: LINEAR YPE: PEPTIDE 26.7%; Score 266; DB 1; Length 224; inilarity 33.8%; Profe No. 1.8e-21; Conservative 21: Migmatches 56: Indels 52:	NAME: BIGGS, SUZANNE L. REGISTRATION NUMBER: 30,158 REFERENCE,DOCKET NUMBER: 203/226 REFERENCE,DOCKET NUMBER: 203/226 TELEEDHONE: (213) 495-1600 TELEFAX: (213) 955-0440 TELEFAX: (213) 955-0440 INFORMATION FOR SEQ ID NO: 85: SEQUENCE CHARACTERISTICS: LERRITH: 224 AMINO ACTOS	FILING DATE: 11-MAY-1993 APPLICATION UNMBER: 08/151,064 FILING DATE: 10-NOVEMBER: 1993 APPLICATION NUMBER: 08/060,433 FILING DATE: 11-MAY-1993 APPLICATION NUMBER: 07/881,721 FILING DATE: 11-MAY-1993 APPLICATION NUMBER: 07/996,972 APPLICATION NUMBER: 07/996,972 FILING DATE: 124-DEC-1992	11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	US-08-458-218-85 US-08-458-218-85 US-08-458-218-85 Sequence 85, Application US/08458218 Fatent No. 5789178 Fatent No. 5789178 FATEL PROPRATION: APPLICATE MATTHEW MOYLE ET AL. TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS NUMBER OF SEQUENCES: 102 CORRESPONDENCE ADDRESS: ADDRESSE: Lyon & Lyon STREET: SHIFE AJON STREET: SHIFE AJON STREET: SHIFE ATON	Db 91 AEKSAYISSARNCSDSSSPPEGDENKYITENSN-NISBAALKAMISWAKEAFHLNKTEEGE 149 Qy 99 GKYYNKNGKTSNIANNYWDSHDKLGCAVVDCSGKTHVVCQYGPE 142

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; MOLECULE TYPE: PEPTIDE US-08-450-497-87
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US-08-450-497-87
                                                                                                                                                                                                                                                                                    TELEFAX: (213) 955-0440
TELEZ: 67-3510
INFORMATION FOR SED ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 224 AMINO ACIDS
TYPE: AMINO ACID
TYPE: AMINO ACID
TOPOLOGY: LINEAR
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Matches
                                                                                                                                                                                            Query Match
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APPLICATION NUMBER: 08/151,064
APPLICATION NUMBER: 08/151,064
APPLICATION NUMBER: 08/151,064
APPLICATION NUMBER: 08/60,433
APPLICATION NUMBER: 07/996,972
APPLICATION NUMBER: 07/986,972
APPLICATION NUMBER: 07/881,721
FILING DATE: 24-DEC-1992
APPLICATION NUMBER: 07/881,721
FILING DATE: 11-MAY-1992
APPLICATION NUMBER: 07/881,721
FILING DATE: 11-MAY-1992
APPLICATION NUMBER: 07/881,721
APPLICATION: NUMBER: 07/881,721
APPLICATION: NUMBER: 07/881,721
APPLICATION: NUMBER: 07/881,721
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: Storage

COMPUTER: 1BM Compatible

OPERATING SYSTEM: 1BM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450,497
                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                            TOPOLOGY:
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  50 LEEKAYKSAEKCSE--EPSSEEENVDVFSAATLNI---PLEAGNSWWSEIFEL-----R 98
                                                                                          210 NKTEGQPIYKVGKPC 224
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                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEKSAYMSARNCSDSSSPPEGDENKYIFENSN-NISEAALKAMISWAKEAFNLNKTEEGE 149
                                                               NDSIRLQFLAMHNGYRSKLALGHISITDESESESDDEYDYWYAPTAPTASKMRYLEYDCE 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/08450497
                                                                                                                                                     Conservative
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ENTION: NOVEL NEUTROPHIL INHIBITORS
                                                                                                                                                26.7%; Score 266; DB 2; Length 224; 33.8%; Pred. No. 1.8e-21; tive 21; Mismatches 56; Indels
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                                                                                                                                                                                                                              Query Match 26.6
Best Local Similarity 32.5
Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: prot-
HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDk...
STREET: 120.
STREET: 120.
TTY: Atlanta
"T: Georgia
USA
USA
USA
345
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DDS/MS-DDS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/419,414
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31, 284
REFERENCE/DOCKET NUMBER: YU
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 424 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
100 KVYNKNG-KTSNIANMYWDSHDKLGCAVVDCSGKTHVVCQYGPEAKGDGKTIYEEGAPCS 158
                                                             287 HGNKCVYQHSHGEDRPGLGENIYKTSVLKFDKNKAAKQASQLWWNELKEFGVGPSNVLTT 346
                                                                                                                                             227 CPSNTGMTDSVRDTFLSVHNEFRSSVARGLEPDALGGNAPKAAKMLKMVYDCEVEASAIR 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210 NKTEGOPIYKVGKPC 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 GVLYRSNHDISNFANLAWDTREKFGCAVVNCPLGEIDGTTIHDGETYATTIHVVCHYPKM 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99
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                                                                                       SAEKCSEEPSSEEE-----NVDVFSAATLNI-----PLEAGNSWWSEIFE------LRG
                                                                                                                                                                                  COOREKLDDDMREMETELHNGYRAAFARNY-----KTSKMRTMVYDCTLEEKAYK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKVYNKNGKTSNIANMVWDSHDKLGCAVVDC------SGKT-----HVVCQYGPE 142
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1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hawdon, John M.
Hotez, Peter J.
Jones, Brian F.
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NO
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                                                                                                                                                                                                                                                 26.6%; Score 265.5; 32.5%; Pred. No. 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pabst
                                                                                                                                                                                                                              27; Mismatches
                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                     Length 424;
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RESULT 14
US-08-173-510B-85
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                                                                                                                                                                                                 Matches
                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 85, Application US/08173510B Patent No. 5747296 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 208 AMINO ACID
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION WITHOUT DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5° Diskette, 1.44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 30,158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 11-MA APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 24-DEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: 3.5" DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                407
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                 111 FGCAVVNCPLGKPDAIITDDEENYATAIHVVCHYPKINKTEGQPIYKVGTPCDDCSEY 168
                               122 LGCAVVDCS-GK-------THVVCQYGPEAKGDGKTIYEEGAPCSRCSDY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       347
                                                                          52
                                                                                                      69
                                                                                                                                                     14 DDDMREMFTELHNGYRAAFARNY--KTSKMRTMYYDCTLEEKAYKSAEKC---SEEPSSE 68
                                                                                                                                                                                               65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      California
                                                                       QCS---PGATC 414
                                                                                                                                 DDD-----YEYGFLPDFAPRASKMRYLEYDCEAEKSAYVSASNCSNISSPPEGY 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RCSDYGAGVTC
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                                                                                                                                                                                          25.6%; Score 255; DB 1; Length 208; Llarity 36.5%; Pred. No. 2.6e-20; Conservative 18; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MATTHEW MOYLE, ET AL.
ENTION: NOVEL NEUTROPHIL INHIBITORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUZANNE
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                                                                                                                                                                                                                                                                                                                                                                                                                        205/073
                                                                                                                                                                                              Indels 40;
                                                                                                                                                                                            Gaps
RESULT 16
US-08-450-497-85
; Sequence 85, Application US/08450497
; Patent No. 5919900
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WOLECULE TYPE: US-08-458-218-83
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US-08-458-218-83
                                                                                                                                                                                                                                      Query Match 25.6
Best Local Similarity 36.5
Matches 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 08/151,064
APPLICATION NUMBER: 08/160,064
FILING DATE: 10-NOVEMBER: 1993
APPLICATION NUMBER: 08/060,433
APPLICATION NUMBER: 07/881,721
FILING DATE: 11-MAY-1992
APPLICATION NUMBER: 07/996,972
FILING TATE: 11-MAY-1992
APPLICATION NUMBER: 07/996,972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
SOFTMARE: WOTO PARFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/458,218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MATTHEW MOYLE ET AL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 20
RELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 633 West F1
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                            LENGTH: 208 AMINO ACIDS TYPE: AMINO ACID TOPOLOGY: LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
111 FGCAVVNCPLGKPDATITDDEENYATATHVVCHYPKINKTEGQPIYKVGTPCDDCSEY 168
                                     122 LGCAVVDCS-GK------THVVCQYGPEAKGDGKTIYEEGAPCSRCSDY 163
                                                                                                                    69 EENVDVFSAATLNI---PLEAGNSWWSEIFEL----RGKVYNKNGKTSNIANMVWDSHDK 121
                                                                                                                                                                                                14 DDDMREMFTELHNGYRAAFARNY--KTSKMRTMVYDCTLEEKAYKSAEKC---SEEPSSE 68
                                                                                                                                                            3 DDD-----YEYGFLPDFAPRASKMRYLEYDCEAEKSAYVSASNCSNISSPPEGY 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3, Application US/08458218 5789178
                                                                              DENKYIFENSN-NISEAALKAMISWAKEAFNLNKTGEGVLYRSNLTISNFANLAWDTREK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                67-351
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3 West Fifth Street
                                                                                                                                                                                                                                                                                                                                              PEPTIDE
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                                                                                                                                                                                                                                                        25.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             83:
                                                                                                                                                                                                                                        18;
                                                                                                                                                                                                                                        Score 255; DB 1; 1
Pred. No. 2.6e-20;
8; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM P.C. DOS 5.0
                                                                                                                                                                                                                                                                           Length 208;
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RESULT 17
US-07-930-686-10
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Sequence 10, Application US/07930686
Patent No. 5525508
GENERAL INFORMATION:
APPLICANT: Sharp, Phillip J
APPLICANT: Wedland, Barry M
APPLICANT: Cobon, Gary S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEG ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 AMINO ACIDS
TYPE: AMINO ACID
TYPE: AMINO ACID
TOPOLOGY: LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/060,433
FILING DATE: 11-MAY-1993
APPLICATION NUMBER: 07/996,972
FILING DATE: 24-DEC-1992
APPLICATION NUMBER: 07/881,721
APPLICATION NUMBER: 07/881,721
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C.
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENERAL INFORMATION:
APPLICANT: MATTHEW
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/173,510 FILING DATE: 23-DEC-1993 APPLICATION NUMBER: 08/151,064 FILING DATE: 10-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                         122 LGCAVVDCS-GK------THVVCQYGPEARGDGKTIYEEGAPCSRCSDY 163
                                                                                                                                                                                                    111 FGCAVVNCPLGKPDAIITDDEENYATAIHVVCHYPKINKTEGQPIYKVGTPCDDCSEY 168
                                                                                                                                                                                                                                                                                                                                                                                            14 DDDMREMFTELHNGYRAAFARNY--KTSKMRTMYYDCTLEEKAYKSAEKC---SEEPSSE 68
                                                                                                                                                                                                                                                                               52 DENKYIFENSN-NISEAALKAMISWAKEAFNLNKTGEGVLYRSNLTISNFANLAWDTREK 110
                                                                                                                                                                                                                                                                                                                     69 EENVDVFSAATLNI---PLEAGNSWWSEIFEL----RGKVYNKNGKTSNIANMYWDSHDK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                      55.6%; Score 255, DB 2; Length 200; Similarity 36.5%; Pred. No. 2.6e-20; Conservative 18; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                           DDD-----YEYGFLPDFAPRASKWRYLEYDCEAEKGAYVSASNCSNISSPPEGY 51
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"ENTION: NOVEL NEUTROPHIL INHIBITORS
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US-08-460-998-10
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; TOPOLOGY: linear ; MOLECULE TYPE: protein US-07-930-686-10
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TELEX: 899149
INFORMATION FOR SEG ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 28.5
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MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURERNY AFPLICATION DATA:
APPLICATION UNMER: US/07/930,686
FILING DATE: 1921106
CLASSIFFICATION DATA:
APPLICATION NUMBER: AU PK4486
APPLICATION NUMBER: AU PK4486
FILING DATE: 06-FEB-1991
RICK APPLICATION DATA:
APPLICATION NUMBER: PCT/AU92/00040
PTILING DATE: 06-FEB-1991
FRICK APPLICATION DATA:
APPLICATION NUMBER: PCT/AU92/00040
PTILING DATE: 06-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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NAME: BENT, Stephen A
REGISTRATION NUMBER: 29,768
TELECOMMUNICATION INFORMATION:
TELEPEAX: (703) 85-9300
TELEFEAX: (703) 683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                 quence 10, Application US/08460998
tent No. 5942413
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CORRESPONDENCE ADDRESS: Foley and Lardner ADDRESSEE: Foley and Lardner
                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                           APPLICANT: Sharp, Phillip J
APPLICANT: Wagland, Barry M
APPLICANT: Cobon, Gary S
TITLE OF INVENTION: Nematode Vaccine
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: United
ZIP: 22313-0299
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CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            442 CTCSRD--EGICV 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     382 SKYSQLAWQSSDRIGCVVVPCWSSWTVVVCEYNPGGDLPGEAIYDVGDPCTKDADCQCPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109 SNIANWYWDSHDKLGCAVVDC-SGKTHVVCQYGPEAKGDGKTIYEEGAPCSRCSDYGA-G 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   322 FGLNTAAMLKRWGNNMHMMSSKANNKTEAAAEAVAAWFGDLOKYGVPENNVFTMNVYTTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 LODDMREMETELHNGYRAAFARNY---------YESKMRIMYYDOTLEEKAYKSAEKCS 62 ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 EEPSSEE------ENVDVFSAATLN---IPLEAGNSWWSEIFEL---RGKVYNKNGKT-- 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Foley and Lardner guite 500, 1800 Diagonal Road
E: Foley and Lardner
suite 500, 3000 K Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10:
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FILING DATE: 00-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A
REGISTRATION UNMER: 29 768
FELECOMMUNICATION INFORMATION:
FELEPANKE: (202) 672-5390
FELEPANKE: (202) 672-5399
FELEX: 904136
INFORMATION FOR SED ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 4454 amino acids
TYPE: Amino acids
                                                                                                                                                                                                                      RESULT 19
US-08-173-510B-89
Commonce 89; Application US/08173510B
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Best Local S
Matches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                               NERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,686
FILING DATE: 06-OCT-1992
                                                                                                                                                                    PPLICANT: MATTHEW MOYLE, ET AL.
ITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 05-JUI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                 DRESSEE
                                                                                                                                                                                                                                                                                                                                                                                                                      109 SNIAMWWIJSHDKIGCAVVDC-SGKTHVVCQVGPEAKGDGKTYEEGAPCSRCSDYGA-G 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            322 FGLNTAAMLKRWGNNMHMMSSKANNKTEAAAEAVAAWFGDLQKYGVPENNVFTMNVYTTL 381
                                                                                                                                                                                                                                                                                                                                                 442 CTCSRD--EGLCV 452
                                                                                                                                                                                                                                                                                                                                                                                   167 VTCDDDWQNLLCI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 EEPSSEE-----ENVDVFSAATLN---IPLEAGNSWWSEIFEL---RGKVYNKNGKT-- 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 20.6%; Score 205; DB 2; Length 454;
1 Similarity 28.5%; Pred, No. 2.7e-14;
55; Conservative 36; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington
: DC
90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RY: United States of America 20007-5109
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LICATION DATA:
TION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATION DATA:
                                                                            Suite
                                                                                       Lyon & Lyon
West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUN-1995
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TELERAX: (213) 955-0440

INFORMATION FOR SEQ ID NO: 89

SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
189 AMINO ACID
TYPE: AMINO ACID
TOPOLOGY: LINEAR
JOPOLOGY: LINEAR
OSCILL TYPE: PEPTIDE
US-08-173-510B-89
                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 20
US-08-458-218-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 20.1%; Score 200; DB 1; Length 189; Best Local Similarity 32.9%; Pred. No. 2.7e-14; Matches 50; Conservative 16; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/151,064

FILING DATE: 10-NOV-1993

APPLICATION NUMBER: 08/060,433

FILING DATE: 11-MAY-1993

APPLICATION NUMBER: 07/996,972

FILING DATE: 24-DEC-1992

APPLICATION NUMBER: 07/881,721

APPLICATION NUMBER: 07/881,721

ATTORNEY/AGENT INFORMATION:

NAME: RIGGS: SUTANMET.
                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
                                                                                                                                                             STREET: 633 new STREET: Suite 4700 CITY: Los Angeles STATE: California
                                                                                                                                                                                                                                                                    APPLICANT: MATTHEW MULLS AT THE OF INVESTIGATE NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
CORRESPONDENCE TO FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C.
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 20:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 23-DE
OPERATING SYSTEM:
SOFTWARE: Word Perfect 5.1
                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98 RGKVYNKNGKTSNIANMVWDSHDKLGCAVVDC 129
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                                                                                                                                                                                                                                                                                                                                                                                                     /, Application US/08458218 5789178
                                                                                                                                                                                                                                            533 West Fifth Street
                                                                                                                                                        U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-DEC-1993
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                       IBM P.C. DOS 5.0
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APPLICATION DATA:

ION NUMBER: 0

ON NUMBER

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OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: WOR'D PERfect 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,497 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 EGYLYRSNLTISNFANLAWDTREKFGCAVVKC 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89, Application US/08450497
5. 5919900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION DATA:
CATION NUMBER: US/08/458,218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8: Lyon & Lyon
633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ON NUMBER: 08/151,064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MATTHEW MOYLE, ET AL.
ENTION: NOVEL NEUTROPHIL INHIBITORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.1%; Score 200; DB 1; Length 189; 32.9%; Pred. No. 2.7e-14; tive 16; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                   Diskette, 1.44 Mb
08/173,510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08/060,433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /996,972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46; Indels 40;
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SEQUENCE CHARACTERISTICS:
LEUCTH: 189 AMINO ACIDS
TYPE: AMINO ACID
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
US-08-450-497-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 22
US-07-930-686-12
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Best Local Similarity 32.9
Matches 50; Conservative
                                                                                                                                                                                                                                                                                              COUNTRY: UHACLE COUNTRY: UHACLE COUNTRY: 2313-029
ZIP: 2313-029
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Flore
MEDIUM TY
                                                                                                                                                                                        COMPUTEK: PC-DOS
OPERATING SYSTEM: PC-DOS
SOPTWARE: PATENTIN Relea
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
APPLICATION INDEER: US,
TITTING DATE: 19921006
            FILING DALLING CLASSIFICATION: SL-
CLASSIFICATION DATA:
PRIOR APPLICATION UNMBER: AU PK4486
APPLICATION UNMBER: AU PK4486
APPLICATION OFFEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: suite 500
CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 205/073
LECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157 EGYLYRSNLTISNFANLAWDTREKFGCAVVKC 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 RGKVYNKNGKTSNIANMVWDSHDKLGCAVVDC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 LEEKAYKSAEKCSEE----PSSEEENVDVF-SAATLNIPLEAGN----SWWSEIFEL---- 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 DSIRLQFLAMHNGYRSNLALGHIGISKESIGDDYDDDYYYFYSSYAPMASKMRYLEYDCD 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/07930686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      suite 500, 1800 Diagonal Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ON NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-DEC-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-DEC-199:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-MAY-199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Phillip J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gary S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nematode Vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.1%; Score 200; DB 2; 32.9%; Pred. No. 2.7e-14; tive 16; Mismatches 46
                                                                                                                                                                                                                                                                                                               Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08/151,064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40;
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08-450-497-89

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Di

APPLICATION DATA:

COUNTRY: U

U.S.A.

Los Angeles California

DDRESSEE:

US-08-458-218-87

MOLECULE TYPE: PEPTIDE

INFORMATION FOR SEQ ID NO: 87:

TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600

SUZANNE 24 - DEC - 1992 11-MAY-:

30, 158

CATION NUMBER

TELEFAX:

(213) 955-0440 DOCKET NUMBER:

SEQUENCE CHARACTERISTICS:

LENGTH: 189 AMINO ACIDS TYPE: AMINO ACID TOPOLOGY: LINEAR

Query Match
Best Local Similarity 32.9
Conservative

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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 440 amino acids
TYPE: AMINO ACID
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-930-686-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 23
US-08-460-998-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 19.8%; Score 197.5; DB 1; Best Local Similarity 27.7%; pred No. 1.8e-13; Matches 57; Conservative 35; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local 9
PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU PK4486

PILING DATE: 06-FEB-1991

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: PCT/AU92/00040

PILING DATE: 06-FEB-1992

ATTORNEY_AGENT INFORMATION:

NAME: Bent, Stephen A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 06-FEB-192
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A .
REGISTRATION NUMBER: 29,768
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEPAX: (703) 633-4109
                                                                                                                                          FILING DATE: U3-U4:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,686
APPLICATION NUMBER: 06-007-1992
                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,998
FILLING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley and Lardner
STREET: suite 500, 3000 K Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX:
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id, Barry M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gary S
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CT-US96-07709-33
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PCT-US96-07709-33
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                                                                                                                                TELEFAX: (303) 863-02
INFORMATION FOR SEQ ID NO:
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 440 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acid
                                                                                                                                                                         TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release $1.0.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: CONNEIL, GAIY J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tripp, Cynthia A. APPLICANT: Wisnewski, Nancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEPAX: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Sheridan Ross & McIntosh STREET: 1700 Lincoln St., Suite 3500 CITY: Denver STATE: Colorado COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US96/07709 FILING DATE: 23-MAY-1996 CLASSIFICATION:
                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LE OF INVENTION: PARASITIC HELMINTH VENOM ALLERGEN LE OF INVENTION: ANTIGEN 5-LIKE GENES AND PROTEINS
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amino acid
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                    protein
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) 863-0223
NO: 33:
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Pred. No. 1.8e-13;
5; Mismatches 77;
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Matches

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RESULT 25
PCT-US96-07709-30
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TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-07709-30
                                                                                                                                                              Query Match
Best Local Similarity 26.4
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 30, Application PC/TUS9607709
GENERAL INFORMATION:
APPLICANT: Tipp, Cynthia A.
APPLICANT: Wisnewski, Nancy
TITLE OF INVENTION: APRISTITC HELMINTH VENOM ALLERGEN
TITLE OF INVENTION: ANTIGEN 5-LIKE GENES AND PROTEINS
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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INFORMATION FOR SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 220 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, vor RRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US96/07709 FILING DATE: 23-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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183 PC 184
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28 ERKKIVGQNNKYRSDLINGKLKNRNGTYMPRGKNMLELRWDCKLESSAQRWANQCIFGHS 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 PSSEEENV--DVF------SAATLNIPLEAGNSWWSEIFELRGKVYNKNGKTS 109
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                                                                                                                               QREKLDDDMREMFTELHNGYRAAFARNY--KTSKMRTMVYDCTLEEKAYKSAEKC--SEE 64
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Y: U.S.A.
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                                                                                                                                                                        15.5%; Score 155; DB 5; Length 220; 26.4%; Pred. No. 3.2e-09; ative 24; Mismatches 68; Indels
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                                                                                                                                                                        Indels 42; Gaps
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  RESULT 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein PCT-US96-07709-25
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PCT-US96-07709-25
                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 15.5%; Score 155; DB 5; Length 248; Best Local Similarity 26.4%; Pred. No. 3.8e-09; Matches 48; Conservative 24; Mismatches 68; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIF: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: PCT/US96/07709
FILLING DATE: 23-MAY-1996
FILLING DATE: 23-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION: NAME: Connell, Gary J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: PARASITIC HELMINTH VENOM ALLERGEN TITLE OF INVENTION: ANTIGEN 5-LIKE GENES AND PROTEINS NUMBER OF SEQUENCES: 43
CORRESPONDEMER ASSESS: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tripp, Cyr
APPLICANT: Wisnewski,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1700 Line
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 26
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                                                                                      227 PC
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                                                                                                                                                                                                                                                                                                                                                                                         9 QREKLDDDMREMFTELHNGYRAAFARNY--KTSKMRTMYYDCTLEEKAYKSAEKC--SEE 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 248 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Sheridan Ross & McIntosh
1700 Lincoln St., Suite 3500
                                                                                      228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tripp, Cynthia A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (303)
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RESULT 28
US-09-199-887-1
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                                                                  Sequence 1, Application US/09199887 Patent No. 6071874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08773368 Patent No. 5856130
                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: LENGTH: 270 amino acids TYPE: amino acid STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: lines
IMMEDIATE SOURCE:
CLONE: 1599164
         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Billings, Lucy RJ
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 530 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NOVEL HUMAN PATHOGENESIS-RELATED TITLE OF INVENTION: PROTEIN NUMBER OF SEQUENCES: 6 CORRESPONDENCE ADDRESSE: ADDRESSE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 3174 Por
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-845-4166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                              193 KNSLC 197
                                                                                                                                                                                                                                        174 ONLLC 178
                                                                                                                                                                                                                                                                                140 IGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQCP---SGYHC---- 192
                                                                                                                                                                                                                                                                                                                  122 LGCAVVDCS-----GKTHV----VCQYGPEAKGDGKTIYEEGAPCSRCSDYGAGVTCDDDW 173
                                                                                                                                                                                                                                                                                                                                                               86 GENLFAITDEGMDVPL-AMEEWHHE-----REHYNLSAATCSPGQMCGHYTQVVWAKTER 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 LDDDMREMFTELHNGYRAAFARNYKTSKMRIMVYDCTLE--EKAYKSAEKC--SEEPSSE 68
                                                                                                                                                                                                                                                                                                                                                                                                    69 EENVDVFSAATLNIPLEAGNSWWSEIFELRGKVYNKNGKTSNIANM------VWDSHDK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                              28 LTDEEKRLMVELHNLYRAQVSPT--ASDMLHMRWDEELAAFAKAYARQXRXGHNKERGRR 85
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         Bandman, Olga
Goli, Surya K.
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Goli, Surya K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.1%; Score 151; DB 2; Length 270; 28.6%; Pred. No. 1.2e-08; ative 26; Mismatches 72; Indels 34;
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; Sequence 88, Application US/08173510B; Patent No. 5747296; GEMERAL INFORMATION: APPLICANT: MATTHEW MOYLE, ET AL., ITLE OF INVENTION: NOVEL NEUTROPHII NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS: STREET: 633 West Fifth Street; STREET: Suite 4700
                                                                                                                                                                                                             RESULT 29
US-08-173-510B-88
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US-09-199-887-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 15.1%; Score 151; DB 3; Length 270; Best Local Similarity 28.6%; Pred. No. 1.2e-08; Matches 53; Conservative 26; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Bilings, Lucy RJ
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: PF-0
TELECOMONICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSTER: UBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE:
CLASSTER: US/09/100 77
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IMMEDIATE SOURCE:
CLONE: 1599164
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APPLICATION NUMBER:
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ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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CITY: Palo Alto
STATE: CA
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140 IGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQCP---SGYHC---- 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 EENVDVFSAATLNIPLEAGNSWWSEIFELRGKVYNKNGKTSNIANM------VWDSHDK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 LTDEEKRLMYELHNLYRAQVSPT--ASDMLHMRWDEELAAFAKAYARQXRXGHNKERGRR 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 LDDDMREMFTELHNGYRAAFARNYKTSKMRTMVYDCTLE--EKAYKSAEKC--SEEPSSE 68
                                                                                                  MATTHEW MOYLE, ET AL.

VENTION: NOVEL NEUTROPHIL INHIBITORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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OPERATING SYSTEM: SOFTWARE: WORD PO

LICATION NUMBER:

COUNTRY:

U.S.A.

Los Angeles California

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JUBICA 1. Application ...,
JUBICA 1. Application ...,
Lent No. 5789178
LENERAL INFORMATION:
APPLICANT MATTHEW MOYLE ET AL.
APPLICANT TAVENTION: NOVEL NEUTROPHIL INHIBITORS
                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APELICATION NUMBER: 08/151
FILING DATE: 10-NOV-1993
APPLICATION NUMBER: 08/06
FILING DATE: 11-MAY-1993
APPLICATION NUMBER: 07/98
FILING DATE: 24-DEC-1992
APPLICATION NUMBER: 07/881
FILING DATE: 11-MAY-1992
FILING DATE: 11-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDIUM TYPE: 3.5" Di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49 TLEEKAYKSAEKCSEEPSSE---EENV-----DVFSAATLNIPLEAGNSWWSEIFEL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 EAEKSAYESAKKCQTTASSSTKYDENLQVIEDPRDINHAA-----LKATISWATEAFNL 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 EMEKGFDDAMRLKFLALHNGYRSRLALGHVSITEESEDYDLYDLSYAPTASKMRYLKYDC 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 QQREKLDDDMREMFTELHNGYRAAFARNY------KTSKMRTMVYDC 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.4%;
Similarity 33.6%;
10; Conservative 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMINO ACIDS
                                                                                                                                                                                                    633 West Fifth Street
Suite 4700
  Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 יששבא: US/08/173,510B
23-DEC-1993
N האחדי
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10-NOV-1993
WBER: 08/060,433
                                        Compatible
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; Pred. No. 2.8;
13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05/073
                     IBM P.C. DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 146;
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US-08-450-497-88
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 AMINO ACIDS
TYPE: AMINO ACID
TYPE: LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 14.4%; Score 144; DB 1; Length 146; Best Local Similarity 33.6%; Pred. No. 2.8e-08; Matches 40; Conservative 13; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 88, Application US/08450497 Patent No. 5919900
                  APPLICATION NUMBER: US/08/450,49
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/173,510
FILING DATE: 23-DEC-1993
APPLICATION NUMBER: 08/151,064
FILING DATE: 10-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM COmpatible
COMPUTER: IBM COMpatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 203/226
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Lyon & Ly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/06/
FILING DATE: 11-MAY-1993
APPLICATION NUMBER: 07/08/
FILING DATE: 11-MAY-1992
APPLICATION NUMBER: 07/99/
FILING DATE: 24-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,218
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MATTHEW MOYLE, ET AL.
PITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS
TUMBER OF SEQUENCES: 104
                                                                                                                                                                                                                                                                                                     STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/151,064
FILING DATE: 10-NOVEMBER-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 TLEEKAYKSAEKCSEEPSSE---EENV------DVFSAATLNIPLEAGNSWWSEIFEL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 EMEKGFDDAMRIKFLALHNGYRSRLALGHVSITEESEDYDLYDLSYAPTASKMRYLKYDC 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 QQREKLDDDMREMFTELHNGYRAAFARNY-------KTSKMRTMVYDC 48
                                                                                                                                                                                                                                                                                                                                                                                             E: Lyon & Lyon
633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                 Suite 4700
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08/060,433
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-08-458-218-86

ADDRESSEE:

90071

U.S.A.

Los Angeles California

Matches Query Match

Local

SEQUENCE CHARACT

LENGTH:

TOPOLOGY:

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RESULT 32
US-08-450-944-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IDM PC compatible
COMPUTER: TOM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,944
FILING DATE: 2-MAY-195
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: VERSION OF THE PROPERTY OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 205/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEYA: (213) 489-1600
TELEY: 67-3510
INFORMATION FOR SEQ ID NO: 88:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 14.4%;
Best Local Similarity 33.6%;
Matches 40; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        equence 5, Application tent No. 5789194 GENERAL INFORMATION:
                                                                                                                                                                                             TELEFAX: (303) 863-0223
NFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                   TELECOMMUNICATION
TELEPHONE: (303
                                                                                                                 SEQUENCE CHARACTERISTICS LENGTH: 205 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 146 AMINO ACII
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: PARASITIC HELMINTH VENOM ALLERGEN ITLE OF INVENTION: ANTIGEN 5-LIKE GENES AND PROTEINS TWEER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                             NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: 2618-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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APPLICATION NUMBER: 07/9
FILING DATE: 24-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PILING DATE: 24-DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5, Application US/08450944
5. 5789194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 EAEKSAYESAKKCQTTASSSTKYDENLQVIEDPRDINHAA-----LKATISWATEAFNL 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 TLEEKAYKSAEKCSEEPSSE---EENV-----DVFSAATLNIPLEAGNSWWSEIFEL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 EMEKGFDDAMRLKFLALHNGYRSRLALGHVSITEESEDYDLYDLSYAPTASKMRYLKYDC 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 QQREKLDDDMREMFTELHNGYRAAFARNY------KTSKMRTMVYDC 48
                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Sheridan Ross & McIntosh
1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tripp, Cynthia A. Wisnewski, Nancy
                                                                                                                                                                                                                                                                        (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEPTIDE
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%; Pred. No. 2.8e-08;
13; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /881,721
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TYPE: amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-07709-5
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PCT-US96-07709-5
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                                                                                                                         Query Match
Best Local Similarity 27.0
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                                                                                                                                                                                                                                                                                             TELEPAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 205 amino acids
TYPE:
                                                                                                                                                                                                                                                                                                                                                                                    NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE,DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: PCT/US96/07709
FILING DATE: 23-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: Connell. Garv.T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tripp, Cynthia A. APPLICANT: Wisnewski, Nancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 YFPGGNMVKDLIYELGNPCKHNKDCRTKRCS 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 KTYSDNPSNNLTSEVAMENILHFTQMAWGETYKLG-----SGVDHNIVMVARTLVFICH 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 KVYN---KNGKTSNIA-----NMVWDSHDKLGCAVVDCSGKTH------VVCQ 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 YGPEAKGDGKTIYEEGAPC-----SRCS 161
57 SAEKC--SEEPSSEE----ENVDVF-------SAATLNIPLEAGNSWWSEIFELRG 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 WANMCVFGHSPSSERRGIGENVYAYWSSGSVRDLKKTAGT----DAGRLWWSEL----E 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 SAEKC--SEEPSSEE----ENVDVF------SAATLNIPLEAGNSWWSEIFELRG 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 CEGGKLTPTERKNIVTQI-NKYRSRLIRGKLKNKDGYLMPKGKNMLRMRWDCKLEKSAQN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 CQQREKLDDDMREMFTELHNGYRAAFARNY------KTSKMRTMVYDCTLEEKAYK 56
                                                            3 CEGGKLTPTERKNIVTQI-NKYRSRLIRGKLKNKDGYLMPKGKNMLRMRWDCKLEKSAQN 61
                                                                                                 7 CQQREKLDDDMREMFTELHNGYRAAFARNY-----KTSKMRTMVYDCTLEEKAYK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application PC/TUS9607709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Sheridan Ross & McIntosh
1700 Lincoln St., Suite 3500
                                                                                                                                                         14.18; 27.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PARASITIC HELMINTH VENOM
ANTIGEN 5-LIKE GENES AND
                                                                                                                                          17;
                                                                                                                                                                                                                                                                                                                                                                                                                                   2618-30-PCT
                                                                                                                                          Score 141; DB 5; Length 205; .Pred. No. le-07; 7; Mismatches 65; Indels
                                                                                                                                          65; Indels 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALLERGEN
PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72;
                                                                                                                                          Gaps
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TELEPHONE: (303) 863-9700

TELEFAX: (303) 863-9723

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 221 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-450-944-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 34
US-08-450-944-2
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APPLICANT: Tipp, Cypthia A.

APPLICANT: Wisnewski, Nancy

TITLE OF INVENTION: PARASITIC HELMINTH VENOM ALLERGEN

TITLE OF INVENTION: ANTIGEN 5-LIKE GENES AND PROTEINS

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sheridan Ross & McIntosh

STREET: 1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER. ITS (06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.455.06.45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1700 Linc
CITY: Denver
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459 REFERENCE/DOCKET NUMBER: 2618-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/450,944 FILING DATE: 23-MAY-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 80203
                                                                                  183
                                                                                                                                                                                                                                                                          100 KYYN---KNGKTSNIA-----NMVWDSHDKLGCAVVDCSGKTH-----VVCQ 138
                                                                                                                                                                                                         129 KYYSDNPSNNLTSEVAMENILHFTQMAWGETYKLG-----SGVDHNIVMVARTLVFICH 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139 YGPEAKGDGKTIYEEGAPC----SRCS 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 KYYSDNPSNNLTSEVAMENILHFTQMAWGETYKLG-----SGVDHNIVMVARTLVFICH 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 YFPGGNMVKDLIYELGNPCKHNKDCRTKRCS 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19
                                                                                                                                                                                                                                                                                                                                                78 WANMCVFGHSPSSERRGIGENVYAYWSSGSVRDLKKTAGT-----DAGRLWWSEL----E 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 COOREKLDDDMREMFTELHNGYRAAFARNY------KTSKMRTMYYDCTLEEKAYK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 14.1%; Score 141; DB 1; Length 221; Isimilarity 27.0%; Pred. No. 1.1e-07; 57; Conservative 17; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 WANMCVFGHSPSSERRGIGENVYAYWSSGSVRDLKKTAGT-----DAGRLWWSEL----E 112
                                                                         YFPGGNMVKDLIYELGNPCKHNKDCRTKRCS 213
                                                                                                                                       YGPEAKGDGKTIYEEGAPC-----SRCS 161
                                                                                                                                                                                                                                                                                                                                                                                                                  SAEKC--SEEPSSEE----ENVDVF------SAATLNIPLEAGNSWWSEIFELRG 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CEGGKLTPTERKNIVTQI-NKYRSRLIRGKLKNKDGYLMPKGKNMLRMRWDCKLEKSAQN 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08450944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 72; Gaps
                                                                                      Sequence 112, Application US/07t Patent No. 5958/84;
GENERAL INFORMATION:
APPLICANT: Benner, Steven A. TITLE OF INVENTION: Prediction NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                            RESULT. 36
US-07-857-224B-112
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PCT-US96-07709-2
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REGISTRATION NUMBER: 32,20

REFERENCE_POCKET NUMBER: 2618

TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700

TELEPAX: (303) 863-9700

INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARCITERISTICS:
LENGTH: 221 mino acids
TYPE: mmino acid
TYPE: mmino acid
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Best Local Similarity
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MEDING TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Tripp, Cynthia A.
APPLICANT: Wisnewski, Nancy
TITLE OF INVENTION: PARASITIC HELMINTH VENOM ALLERGEN
TITLE OF INVENTION: ANTIGEN 5-LIKE GENES AND PROTEINS
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1700 Linc
CITY: Denver
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 23-MF CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U
                                                                 DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 YFPGGNMVKDLIYELGNPCKHNKDCRTKRCS 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             139 YGPEAKGDGKTIYEEGAPC-----SRCS 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 KYYSDNPSNNLTSEVAMENILHFTQMAWGETYKLG-----SGVDHNIVMVARTLVFICH 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 KYYN---KNGKTSNIA-----NMYWDSHDKLGCAYVDCSGKTH------VVCQ 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 WANMCVFGHSPSSERRGIGENVYAYWSSGSVRDLKKTAGT-----DAGRLWWSEL----E 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 CEGGKLTPTERKNIVTQI-NKYRSRLIRGKLKNKDGYLMPKGKNMLRMRWDCKLEKSAQN 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 COOREKLDDDMREMFTELHNGYRAAFARNY-----KTSKMRTMVYDCTLEEKAYK 56
SEE: Steven A. Benner
: Hadlaubstrasse 151
Zurich
                                                                                                                                                                                                                                                                                                               Application US/07857224B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.1%; Score 141; DB 5; Length 221; 27.0%; Pred. No. 1.1e-07;
                                                                                                                                               Steven A.
Predicting Folded Structures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Release #1.0, Version #1.25
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US-08-773-368-4
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US-07-857-224B-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 12.7%; Score 127; DB 2
Best Local Similarity 26.9%; Pred. No. 2e-06;
Matches 39; Conservative 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: none
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Apple MacIntosh 7.0 OPERATING SYSTEM: MACINTOSh 7.0 SOFTWARE: Microsoft Word CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VOLUME: 5
PAGES: 527-534
PATE: 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: human
FEATURE: Testis specific protein; Table 17 Row 8
FUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: (note: this is
COMPUTER READABLE FORM:
                                                                                                                                                                                            ant No.
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DESCRIPTION: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                          DDRESSEE:
                                                                                                                                                                                                                                                                                                      112 CPAGNNMNRKNTPYQQGTPCAGCPD 136
                                                                                                                                                                                                                                                                                                                          140 GPEAKGDGK--TIYEEGAPCSRCSD 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38 TSKMRTMVYDCTLEE----KAYKSAEKCSE-----EPSSEEENVDVFSAATLNIPLEAGN 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 TINAQRWANKCTLQHSDPEDRKTSTRCGENLYMSSDPTS-----WSSAI------ 54
    Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                SWYDEILDF---VYGVGPKSPNAVVGHYTQLVWYSTYQVGCGIAYCPNQDSLKYYYVCQY 111
                                                                                                                                                                                                                                                                                                                                                                                                                SWWSEIFELRGKVYNKNGKTSN-----IANMYWDSHDKLGCAVVDC----SGKTHVVCQY 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s: Spurr, N.

Cloning and mapping of a testis-specific gene with sequence similarity to a sperm coating glycoprotein gene

: Genomics
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                                                                                                                                                                                                            Application US/08773368
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Gutknecht, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brew, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (International) 41 1 632 2830 (International) 41 1 262 2437
                                                                                                                                                      Bandman, Olga
                                        ncyte Pharmaceuticals, Inc
                      Porter Drive
                                                                                                                             Surya
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inch diskette, 1.4 Mb storage
                                                                                                              NOVEL HUMAN PATHOGENESIS-RELATED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45; Indels 38;
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; LIBRARY: GenBank
; CLONE: 1030053
US-08-773-368-4
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Matches
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Best Local Similarity 24.9%;
Matches 49; Conservative 30
                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 266 amino acids
                                                                                                                                                                                                                                                                ent No.
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/773,368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Billing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Billings, Lucy RJ
RECISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
ELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                 STATE: CA
                                                                                                                                                                      TPLICANT: GOL1, SUTYA K.
TPLE OF INVENTION: NOVEL HUMAN PATHOGENESIS-RELATED
TIE OF INVENTION: PROTEIN
                                                                                         RRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                              198 ----- NDKCLDNLCV 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 QVVWADSYKVGCAVQFCPKVSGFDALSNGAHFICNYGP -- GGNYPTWPYKRGATCSACPN 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 NMYWDSHDKLGCAVVDC-----SGKTHVVCQYGPEAKGDGKT-IYEEGAPCSRCSD 162
                                                                                                                                                                                                                                                                                                                                                                                                                  163 YGAGVTCDDDWQNLLCI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88 KLHPNFTSLGENIWTGSVPIFSVSS-----AITNWYDEIQDYDFKTRICKK--VCGHYT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 -----SSEEEN-----VDVFSAATLNIPLEAGNSWWSEI--FELRGKVYNKNGKTSNIA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 NEDFIKDCVRIHNKFRSEVKPT--ASDMLYMTWDPALAQIAKAWASNCQFSHNTRLKPPH 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 DDDMREMFTELHNGYRAAFARNYKTSKMRTMYYDCTLEEKAYKSAEKCS-----EEP- 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                  Application US/09199887
                                      USA
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                                                                                                                                                                                                                                01ga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 50;
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PPLICANT: Bandman, Olga
PPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN PATHOGENESIS-RELATED
TITLE OF INVENTION: PROTEIN
TUMBER OF SEQUENCES:

TO THE PROTECT OF SEQUENCES:

TO THE PROTECT OF SEQUENCES:

TO THE PROTECT OF SEQUENCES:
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 -----SSEEEN-----VDVFSAATLNIPLEAGNSWWSEI--FELRGKVYNKNGKTSNIA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 DDDMREMETELHNGYRAAFARNYKTSKMRTMYYDCTLEEKAYKSAEKCS-----EEP- 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88 KLHPNFTSLGENIWTGSVPIFSVSS-----AITNWYDEIQDYDFKTRICKK--VCGHYT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 12.2%; Score 122; DB 3; Similarity 24.9%; Pred. No. 1.9e-05; 49; Conservative 30; Mismatches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NMVWDSHDKLGCAVVDC-----SGKTHVVCQYGPEAKGDGKT-IYEEGAPCSRCSD 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEDFIKDCVRIHNKFRSEVKPT--ASDMLYMTWDPALAQIAKAWASNCQFSHNTRLKPPH 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QVVWADSYKVGCAVQFCPKVSGFDALSNGAHFICNYGP--GGNYPTWPYKRGATCSACPN 197
                                                                                                                                                                                                           E: Incyte Pharmaceuticals, Inc 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FastSEQ for Windows Version 2.0
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Best Local Similarity
Matches 49; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 847722
                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FasteEQ for Mindows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/773,368
                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
ADDRESSEE: Incyte P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              ITLE OF INVENTION: NOVEL HUMAN PATHOGENESIS-RELATED
                                                                                                                                                                                                                                                 CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Billings, Lucy RJ
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
LECOMOUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188 -----NDKCLDNLCV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 VWADSYKYGCAYOFCPKYSGFDALSNGAHFICNYGP--GGNYPTWPYKRGATCSACPN-- 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 VWDSHDKLGCAVVDC------SGKTHVVCQYGPEAKGDGKT-IYEEGAPCSRCSDYG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 -----SSEEEN-----VDVFSAATLNIPLEAGNSWWSEIFELRGKVYNKNGKTSNIANM 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 DDDMREMFTELHNGYRAAFARNYKTSKMRTMYYDCTLEEKAYKSAEKCS-----EEP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 KLHPNFTSLGENIWTGSVPIFSVSS-----AITNWYDEIQDYNFKTRICKKVCGHYTQV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 NEDFIKDCVRIHNKFRSEVKPT--ASDMLYMTWDPALAQIAKAWASNCQFSHNTRLKPPH 77
                                                                                                                                                                                                           94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGVTCDDDWQNLLCI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/09199887
                                                                                                                                                                                                                                                                                                  E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bandman, Olga
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Lucy RJ
26,749
PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.1%; Score 121; DB 2; Length 219; 25.1%; Pred. No. 1.8e-05; tive 26; Mismatches 74; Indels 46;
                                              as/09/199,887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ω
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IMPOLOGY: 11near
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1030053

Local

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INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 266 amino acids

amino acids

NAME: Billings, Lucy RJ
REGISTRATION NUMBER: 36,749
REFERENCE_DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555

415-845-4166

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/199,887

IBM Compatible YSTEM: DOS Diskette

PRIOR APPLICATION DATA: 08/773,368

NEY/AGENT INFORMATION:

S 문

198 ----- NDKCLDNLCV 207 163 YGAGYTCDDDWQNLLCI 179

RESULT 39 US-08-773-368-3

Application US/08773368

COMPUTER READABLE FORM: MEDIUM TYPE: Diskett

IBM Compatible

CORRESPONDENCE ADDRESS

ADDRESSEE:

Palo Alto

USA

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US-07-857-2248-111
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TELEX: none INFORMATION FOR SEQ ID NO: 111:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 219 amino acid
                                                                                                                                                                                 CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                ZIP: (note: this is an international post code) CH-8092 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
                                                                                 CLASSIFICATION: 436
PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIBRARY: GenBa
CLONE: 847722
                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PETELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                 STREET: Hadla
CITY: Zurich
STATE: none
                                                                                                                                                                                                                                                                                                                                                                                                                                          PPLICANT: Benner, Steven A.

ITLE OF INVENTION: Predicting Folded Structures of Proteins

ORDER OF SEQUENCES: 114
                                                                                                                                                                                                                       COMPUTER: Apple MacIntosl
OPERATING SYSTEM: MacInto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 219 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                        APPLICATION NUMBER: UPPLING DATE: 03/25/92
                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 ----NDKCLDNLCV 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111, Application US/07857224B
5. 5958784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 DDDMREMFTELHNGYRAAFARNYKTSKMRTMYYDCTLEEKAYKSAEKCS-----EEP- 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 -----SSEEEN-----VDVFSAATLNIPLEAGNSWWSEIFELRGKVYNKNGKTSNIANM 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 NEDFIKDCVRIHNKFRSEVKPT--ASDMLYMTWDPALAQIAKAWASNCQFSHNTRLKPPH 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VWADSYKVGCAVQFCPKVSGFDALSNGAHFICNYGP--GGNYPTWPYKRGATCSACPN-- 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VWDSHDKLGCAVVDC-----SGKTHVVCQYGPEAKGDGKT-IYEEGAPCSRCSDYG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLHPNFTSLGENIWTGSVPIFSVSS-----AITNWYDEIQDYNFKTRICKKVCGHYTQV 131
                                                                                                                                                                                                                                                                                                                                                                                     E: Steven A. Benner
Hadlaubstrasse 151
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linear
URCF
                                        (International) 41 1
                                                                                                                                                                                                                                                                                                                            Switzerland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenBank
                                                                                                                                                                                                 SYSTEM: MacIntosh 7.0
Microsoft Word
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MRER: 36,749
                                                                                                                                                                                                                                                             inch diskette, 1.4 Mb storage
                                                                                                                                                              US/07/857,224B
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US-07-857-224B-111
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US-08-614-935-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 11.5
Best Local Similarity 28.0
Matches 35; Conservative
                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/MS/614,935
FILING DATE: 11-MAR-1996
CLASSIFICATION: 436
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION: King,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          quence 5, Application US/08614935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DESCRIPTION: protein ORIGINAL SOURCE:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-156
TELECOMMUNICATION INFORMATION:
                                                           ATTORNEY/AGENT INFORMATION: NAME: Jackson Esq., Dav1
                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE: testis specific protein; Table 17 ROW PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 137
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: King, Te P.
FITLE OF INVENTION: IMMUNOMORE
FITLE OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 81
                                                                                                                                                                                                                                                                                                                      CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAGES: 527-534
DATE: 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                       DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 KTSNIA-----NMYWDSHDKLGCAVVDCSGKTHV----VCQYGPEAKGDGK--TIYEEGA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 AKPNSAVGHYTQLVWYSSFKIGCGIAYCPNQDNLKYFYVCHYCPMGNNVMKKSTPYQQGT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 AQKWANKCILEHSSKDDR-KINIRCGENLYMSTDPTLWSTVIQ---SWYNENEDFVYGVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 AYKSAEKCSEEPSSEEENVDVFSAATINIPLEAGNSWWSEIFELRGKVYNKN------G 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RS: Spurr, N.
Cloning and mapping c
Similarity to a sperm
AL: Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                                                   Floor
                                                                                                                                                                                                                                                                                                                                                                            3: David A. Jackson, Esq.
411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kasahara, M.
Gutknecht, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.5%; Score 115; DB 2; Length 137; 28.0%; Pred. No. 4.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMUNOMODULATORY PEPTIES OF VESPID
                                                                                                                                                                              Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ping of a testis-specific gene with sequence sperm coating glycoprotein gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49; Indels 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 43
US-09-130-287-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/09130287
PATENT NO. 6106844
GENERAL INFORMATION:
APPLICANT: King, Te P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                  APPLICATION NUMBER: US 08/614,935
FILING DATE: 11-MAR-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Jackson E94, David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-156 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                        TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Floor
STREET: Floor
STREET: Hackensack
""" Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: IMMUNOMODULATORY PEPTIES OF VESPID TITLE OF INVENTION: ANTIGEN 5
                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 07601
ENGTH: 204 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocal
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39; Conservative
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411 Hackensack Ave, Continental Plaza, 4th
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RESULT 44
US-08-614-935-4
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US-08-614-935-4
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                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/614,935
FILING DATE: 11-MAR-1996
CLASSIFICATION: 436
CLASSIFICATION: 436
                                                                                                                                                                                                                                         TELEFAX: 201-343-1684 INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: I
HYPOTHETICAL: NO
              HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Dollchovespula maculata
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                             MOLECULE TYPE: pr
                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Jackson ESG., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
LENGTH: 205 amino aci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: UZIP: 07601
                                                                                                                                                         LENGTH: 205 amino acids TYPE: amino acid STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                              US/08/614,935
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	9-130-287-4 9-130-287-4 9-130-287-4 9-130-287-4 punce 4, Applicat. tent No. 6106844 ERERAL INFORMATION APPLICANT: King, TITLE OF INVENTION TITLE OF INVENTION UMBER OF SEQUENCY CORRESPONDENCE AD ADDRESSEE: Dav STREET: FLOOR STREET: FLOOR COMPUTER READABLE MEDIUM TYPE: FLOOR COMPUTER READABLE COMPUTER READABLE MEDIUM TYPE: FLOOR COMPUTER TEM JOY COMPUTER JOY				y Matc Local hes
• 5	45 30-287-4 30-287-4 30-287-4 30-287-4 30-287-4 RAL INFORMATION: FPLICANT: King, FPLICANT: King, FPLICANT: King, FPLICANT: King, FPLICANT: King, FPLICANT: King, TLE OF INVENTION MEER OF INVENTION MEER OF SEQUENCE: RESPONDENCE ADD ADDRESSEE: Davi STREET: 411 Hack COUNTRY: FLOOT MEDIUM TYPE: MAME: JOACH TELEFAX: 201-34 TELEFAX: 201-34 TELEFAX: 201-34 TELEFAX: 201-34 TYPE: MAMIO ACI STRANTION FOR SEQ OURNCE CHARACTER TYPE: MAMIO ACI STRANTION TOR SEQ OURNCE CHARACTER TYPE: MAMIO ACI STRANTION STRANTION MEDIUM MEDI	106 153	96	13 36	
31m1	7-4 610684 610684 FORMAT FORMA	SK) - GK	FGF	ASA : :	Simi
Similarity 0; Conser	14. Application in the property of the propert	GHY.	DQC .	DEK	Similarity 0; Conser
1ty serv	45 30-287-4 30-287-4 30-287-4 30-287-4 30-287-4 30-287-4 APPLICATION: PLICANT: King, Te p TLE OF INVENTION: TLE OF INVENTION: TLE OF INVENTION: ADDRESSEE: DAVID A: MEBER OF SEQUENCES: RRESPONDENCE ADDRESS STREET: 411 Hackenss STREET: 411 Hackenss CITY: Hackenssck STATE: New Jersey COUNTRY: USA ZIP: 07601 ZIP: O7601 ZIP: Hackenssck STATE: New Jersey COUNTRY: USA ZIP: 07601 ZIP: Hackenssck STATE: NEW JERSEY COUNTRY: USA APPLICATION NUMBER: FILING DATE: IN PAPPLICATION DATA APPLICATION NUMBER: FILING DATE: 11-MAR CLASSIFICATION: 424 IOR APPLICATION DATA APPLICATION NUMBER: FILING DATE: 11-MAR TORNEY/AGENT INFORMA NAME: Jackson Esq. TILEPHONE: 201-431-16 GUENCE CHARACTERISTI TELEPHONE: 201-431-16 GUENCE CHARACTERISTI LENGTH: 205 amino a TYPE: amino acid STRANDEDNESS: sind ON TYPE: OTHER COUNTRY SEGUENT NO AGMENT TYPE: OGNAMINAL SOURCE: ORGANISM: DOIIChove 30-287-4 30-287-4 30-287-4	TQMN	RNTI	EMFT	1ty serv
11. larity 23. Conservative	IN 45 1-130-287-4	WGK	ERYQ	CELH 	1 2 7ati
11.0%; 23.4%; ive	JA 45 Jay 287-4 Jupance 4, Application US/0913 MERLI INFORMATION: APPLICANT: King, Te P. APPLICANT: King, Te P. APPLICANT: King, Te P. TITLE OF INVENTION: IMMUNOM TITLE OF INVENTION: ANTIGEN TITLE OF INVENTION: ANTIGEN TITLE OF INVENTION: ANTIGEN TOTHER OF SEQUENCES: 81 CORRESSORDENCE ADDRESS: ADDRESSEE: David A. Jacks STREET: 411 Hackensack AV STREET: 412 Hackensack AV STREET: Floor COMPUTER: IBM PC COMPATION DETANING SYSTEM: PC-DOS/ COMPUTER: IBM PC COMPATION DETANING SYSTEM: PC-DOS/ SOFTWARE: PAtentin Releas APPLICATION NUMBER: US/09 FILING DATE: CLASSIFICATION NUMBER: US/09 FILING DATE: 11-MAR-196 CLASSIFICATION: 424 APLICATION NUMBER: US/09 FILING DATE: 11-MAR-196 CLASSIFICATION NUMBER: 26,7 REFERENCE/DOCKET NUMBER: 20,7 REFERENCE/DOC	HDKL	VGQI	NGY!	11.0%; ilarity 23.4%; Conservative 3
<u>ω</u>		GG A	EEPSSEEENVDVFSA ; ; TEKYQVGQNVAIASTTGN	LDDDMREMFTELHNGYRAAFARNYKT- : : : : : VSNDEKNEIVNRHNQFRQKVAKGLETR	_
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5; 34;	·	IYE 	NPK	AKI.	••
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Qy 106 GKTSNIAI : :	Db 96 FGHDQCRI	Qу 63	Db 36 VSNDEKNI	Qy 13 LDDDMREI
106 GKTSNIANMVMDSHDKLGCAVVDCSGKTH-VVCQYGPEAKGDGKTIYE 152 	96 FGHDQCRNTEKYQVGQNVAIASTTGNSYATMSKLIEMWENEVKDFNFKKGTIGDNNF 152	63REPSSEEENVDVFSAATLNIPLEAGNSWWSEIFELRGKVYNKN- 105	36 VSNDEKNEIVNRHNDERQKVAKGLETRGNPGPQPPAKNMNVLVWNDELAKIAQTWANQCS 95	

Search completed: July 15, 2003, 08:36:45 Job time : 28 secs

Title: Perfect score: Sequence:

on:

Scoring table:

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OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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997
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Copyright (c) 1993 - 2003 Compugen Ltd.
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  DB
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0 US-09-797-410-3
0 US-09-797-410-2
0 US-09-969-271-3
0 US-09-969-271-644B-6
1 US-10-051-644B-1
1 US-09-808-602-27
1 US-09-808-602-27
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     Sequence 4, Appli
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Sequence 27, Appli
Sequence 28, Appli
Sequence 36, Appli
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Patent No. US2002098179A1

Patent No. US2002098179A1

PERSONANTION:
GENERAL INFORMATION:
APPLICANT: Pfizer Limited (GB and EP (GB) only)
APPLICANT: Pfizer Limited (GB and EP (GB) only)
APPLICANTION: Pharmaceutical Combinations
FIILE OF INVENTION: Pharmaceutical Combinations
FILE REFERENCE: PCS10951APME
CURRENT APPLICATION NUMBER: US/09/969,271

CURRENT FILING DATE: 2001-10-01

PRIOR APPLICATION NUMBER: GB 0025473.0

PRIOR APPLICATION NUMBER: GB 0025473.0

PRIOR APPLICATION WINDER: GB 
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Best Local Similarity 34.3
Matches 69; Conservative
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                                                                                             143 AKGDGKTIYEEGAPCSRCSDY 163
                                                                                                                                             51 EEKAYKSAEKCSEE---PSSEEENVDVFSAATLNI---PLEAGNSWWSEIFEL-----R 98
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                                                               NKTEGOPIYKVGTPCDDCSEY 217
                                                                                                                                                                      GKYYNKNGKTSNIANMYWDSHDKLGCAVVDC-----SGKT----HVVCQYGPE 142
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9 US-09-907-613-285

9 US-09-907-613-285

9 US-09-707-65-360

9 US-10-176-918-360

9 US-10-176-918-360

9 US-10-140-474-360

9 US-09-904-820-285

9 US-09-904-820-285

9 US-09-904-82-285

9 US-09-906-466-285

9 US-09-906-466-285

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9 US-09-903-746-285

9 US-09-903-745-285

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Score

Query Match

115.99 115.99 115.99 115.99 115.99 115.99 115.99

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PRIOR APPLICATION NUMBER: GB 0025473.0
PRIOR FILING DATE: 2000-10-17
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 274
TYPE: PRT
ORGANISM: Ancylostoma caninum (canine hookw
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Patent No. US20020098179A1
GENERAL INFORMATION:
APPLICANT: Pfizer Inc. (All designated States except GB and EP (GB));
TITLE OF INVENTION: Pharmaceutical Combinations
FILE REFERENCE: PCS10951APME
CURRENT APPLICATION NUMBER: US/09/969,271
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: US/09/969,271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Plas, Steven J.
APPLICANT: Zhu, Marie M.
APPLICANT: Zhu, Marie M.
TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF NEUTROPHIL INHIBITORY
TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF NEUTROPHIL INHIBITORY
FILE REFERENCE: SUZANNE L. BIGGS: Corvas 259/001
CURRENT APPLICATION NUMBER: US/09/797,410
CURRENT FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 3
LENGTH: 257
TYPE: PRT
  Best Local
Matches
                                       Query Match
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(257)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 DDDMREMFTELHNGYRAAFARNY--------KTSKMRTMVYDCTL 50
1 Similarity
69; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 34.3
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AKGDGKTIYEEGAPCSRCSDY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NDSIRLQFLAMHNGYRSKLALGHISITEESESDDDDDDFGFLPDFAPRASKMRYLEYDCEA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ho, Lewis
Koehler, Mark A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NKTEGOPIYKVGTPCDDCSEY 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVLYRSNHDISNFANLAWDAREKFGCAVVNCPLGEIDDETNHDGETYATTIHVVCHYPKI 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GKVYNKNGKTSNIANMVWDSHDKLGCAVVDC-----SGKT-----HVVCQYGPE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKSAYMSARNCSDSSSPPEGYDENKYIFENSN-NISEAALKAMISWAKEAFNLNKTKEGE 136
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    Conservative
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Roderick W
  29.1%; Score 290; DB 10; 34.3%; Pred. No. 4.7e-21; tive 23; Mismatches 57;
                                                                                                  caninum (canine hookworm)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 290; DB 10;
; Pred. No. 4.3e-21;
23; Mismatches 57;
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                                       Length 274;
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  Indels 52;
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GENERAL INCOMPANATION

GENERAL INCOMPANATION

APPLICANT: Pluschkell, Stefanie B.

APPLICANT: Geldart, Roderick W.

APPLICANT: Ho, Lewis

APPLICANT: Koehler, Mark A.

APPLICANT: Okediadi. Centy A.

APPLICANT: Plus, Steven J.

APPLICANT: Plus, Steven J.

APPLICANT: Div, Marie M.

ITILE OF INVENTION: PROCESS FOR THE PREPARATION OF NEUTROPHIL INHIBITORY

ITILE OF INVENTION: PACTOR

FILE REFERENCE: SURANNE L. BIGGS: Corvas 259/001

CURRENT APPLICATION NUMBER: US/09/797,410

CURRENT APPLICATION NUMBER: US/09/797,410

SEQ ID NO 2

SEQ ID NO 3

SEQ ID NO 3

SEQ ID NO 2

LENGTH: 274

TYPE: PRI
ORGANISM: Ancylostoma caninum

US-09-797-410-2
Sequence 6, Application US/10051644B
publication No. US20030126025A1
GENERAL INFORMATION:
APPLICANT: L1u, et al.
TITLE OF INVENTION: Screens and Assays for Agents Useful in Controlling
TITLE OF INVENTION: Parasitic Nematodes
FILE REFERENCE: 2002630-0012
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US-09-797-410-2
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Best Local Similarity 34.3%; Pred. No. 4.7e-21;
Matches 69; Conservative 23; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09797410 Patent No. US20020099183A1
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| :|: ||: | || ||:|
214 NKTEGQPIYKVGTPCDDCSEY 234
                                                                                                                                                                                                                                                                                                | :|: ||: | || ||:|
214 NKTEGQPIYKYGTPCDDCSEY 234
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                                                                                                                                                                                                                                                                                                                                                                                                             154 GVLYRSNHDISNFANLAWDAREKFGCAVVNCPLGEIDDETNHDGETYATTIHVVCHYPKI 213
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RESULT 6
US-10-051-644B-3
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TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Clustal W
OTHER INFORMATION: Alignment of VAP-1, VAP-2, and selected other
US-10-051-6448-6

    O'HER INFORMATION: Description of Artificial Sequence: VAP-2 Amino
TOTHER INFORMATION: Acid Sequence
    O'51-644B-3

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Publication No. US20030126625A1
GENERAL INFORMATION:
APPLICANT: Liu, et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/051,644B
CURRENT FILING DATE: 2003-03-04
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 3
LENGTH: 473
TYPE: PRT
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
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CURRENT FILING DATE: 2003-03-04
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 6
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Best Local Similarity 32.5%; Pred. No. 1e-17;
Matches 62; Conservative 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Liu, et al.
TITLE OF INVENTION: Screens and Assays for Agents
TITLE OF INVENTION: Parasitic Nematodes
FILE REFERENCE: 2002630-0012
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence FEATURE:
376 QELEEFGTPIDNVLTPELWDLKGKAIGHYTQMAWDRTTRLGCGIANCPKMSYVVCHYGPA 435
                                                                                           316 MIKMEYDCMLERFAQNWANNCYFAHSAHYERPNQGQNLYMSSFSNPDPRSLIHTAVEKWW 375
                                                                                                                                                                                         256 LCQAPSMVKDDGGSFQCDNSLVSDVTRNFTLEQHNFYRSRLAKGFEWNGETNTSQPKASQ 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 ALWNRPGMQIGHYTQMAWDTTYKLGCAVVFCNDFTFGVCQYGPGGNYMGHVIYTMGQPCS 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188
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                                                       92
                                                                                                                                       41 MRTMVYDCTLEEKAYKSAEKC-----SEEPSSEEENVDVFSAAT---LNIPLEAGNSWW 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 SAEKCSEEPSSEEE----NVDVFSAATLNI-----PLEAGNSWWSEIFE------LRG 99
                                                                                                                                                                                                                                  6 LCQQREKLDDD------KTSK 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 HGNKCVYQHSHGEDRPGLGENIYKTSVLKFDKNKAAKQASQLWWNELKEFGVGPSNVLTT 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 COOREKLDDDMREMFTELHNGYRAAFARNY-----KTSKMRTMVYDCTLEEKAYK 56
                                                                                                                                                                                                                                                                                    n 21.0%; Score 209.5; Similarity 27.2%; Pred. No. 1.1e 59; Conservative 26; Mismatches
                                            SEIFE-----LRGKYYNKNGKT-SNIANMYWDSHDKLGCAVVDCSGKTHVVCQYGPE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QCS---PGATC 195
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                                                                                                                                                                                                                                                                 ..le~12;
nes 87; Indels 45;
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RESULT 8
US-09-808-602-27
: Sequence 27, Application us,
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CURRENT FILING DATE: 2003-03-04
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 425
TYPE: PAT
ORGALISM: Artificial Sequence
FEATURE:
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US-10-051-644B-1
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US-10-051-644B-1
SOFTWARE: Pat
SEQ ID NO 27
LENGTH: 300
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                                                                                  PRIOR APPLICATION NUMBER: 09/800,198
PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 60/186,596
PRIOR FILING DATE: 2000-03-03
NUMBER OF ESE ID NOS: 114
PROFIMARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US
CURRENT FILING DATE: 2001-03-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MacDougall, John
TITLE OF INVENTION: No. US20020155115A1el Proteins and Nuclec
FILE REFERENCE: 15966-697 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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TITLE OF INVENTION: Screens and Assays for Agents Useful in Controlling
TITLE OF INVENTION: Parasitle Nematodes
FILE REFERENCE: 2002630-0012
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Local Similarity 23.0%; Pred. No. 8.4e-11;
es 45; Conservative 40; Mismatches 79; Indels 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 GAPCSRCSDYGAGVTC 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                342 DNILTQAVFDRG--VGHYTQMAWEGTTEIGCFVENCPTFTYSVCQYGPAGNYMNQLIYTK 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      282 EANARTWAKGCLYOHSTSAQRPGLGENLYMISINNMPKIQTAEDSSKAWWSELKDFGVGS 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222 FIMCPSVTDQSDQARQNFLDTHNKLRTSLAKGLEADGIAAGAFAPMAKQMPKLVKYSCTV 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         436 GNRKNNKIYEIGDPCEVDDDCPIGTDCEK--TTSLCV 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 AKGDGKTIYEEGAPCSRCSDYGAGVTCDDDWQNLLCI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 ---LRGKVYNKNGKTSNIANMVWDSHDKLGCAVVDCSGKTHVVCQYGPEAKGDGKTIYEE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 EEKAYKSAEKCSEEPSSEEE----NVDVFSAATLNIPL----EAGNSWWSEIFE----- 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 YSLCQQREKLDDDMREMFTELHNGYRAAFARNYKTSKM-----RTMVYDCTL 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fernandes, Elma
Shimkets, Richard A
Herrman, John L
Majumder, Kumud
Mishra, Vishnu
Mezes, Peter S
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; ORGANISM: Homo sapiens
US-09-808-602-27
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US-09-800-198-25
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                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2.1
SEQ ID 00 25
LENGTH: 300
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                   Matches
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CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 60/186,596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 SAEKCSEE--PSSEEENVDVFSAATLNIPLEAG-----NSWWSEI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43 DGEWWIAKQRGKRAITDNDMQSIL-DLHNKLR---SQVYPTASNMEYMTWDVELERSAES 98
                                                                                                                                                                                                                                             43 DGEWWIAKQRGKRAITDNDMQSIL-DLHNKLR---SQVYPTASNMEYMTWDVELERSAES 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EGDYSLCQQREK----LDDDMREMFTELHNGYRAAFARNYKT-SKMRTMVYDCTLEEKAYK 56
                                                                                                                                                                                                                                                                                    1 EGDYSLCQQREK···LDDDMREMFTELHNGYRAAFARNYKT-SKMRTMYYDCTLEEKAYK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : Mezes, Peter S
: Rastell1, Luca
: INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
                                                                                                                                                                                                                                                                                                                              Similarity 25.5
3; Conservative
                                                                               NPYCPFRCSGPV-----CTHYTQVVWATSNRIGCAINLCHNMNIWGQIWPKAVYLVCNY 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPEAKGDGKTIYEEGAPCSRC-SDYGAG 166
SPKGNWWGHAPYKHGRPCSACPPSFGGG 234
                                     GPEAKGDGKTIYEEGAPCSRC-SDYGAG 166
                                                                                                                      ----FELRGKVYNKNGKTSNIANMVWDSHDKLGCAVVDCSG-----KTHVVCQY 139
                                                                                                                                                              RAESCLWEHGPAS-----LLPSIGQNLGAHWGRYRPPTFHVQSWYDEVKDFSYPYEHEC 152
                                                                                                                                                                                                     SAEKCSEE--PSSEEENVDVFSAATLNIPLEAG-----NSWWSEI------ 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPKGNWWGHAPYKHGRPCSACPPSFGGG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RAESCLWEHGPAS-----LLPSIGQNLGAHWGRYRPPTFHVQSWYDEVKDFSYPYEHEC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shimkets, Richard A
Herrmann, John L
Majumder, Kumud
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; Pred. No. 5.3e
31; Mismatches
                                                                                                                                                                                                                                                                                                                              DB 9; Length 300;
5.3e-08;
hes 66; Indels
                                                                                                                                                                                                                                                                                                                              Indels 58;
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RESULT 10
US-09-905-291A-285
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PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,291A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FLIKK DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/28665
PRIOR APPLICATION NUMBER: PCT/US99/28665
PRIOR FILING DATE: 1999-12-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/145,698 PRIOR FILING DATE: 1999-07-26
                                                                                                PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITLE REFERENCE: 10466-14
URRENT ADDITOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
FILING DATE: 1999-09-15
                                                                                                                                                APPLICATION NUMBER: PCT/US99/30095
FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US99/28214 FILING DATE: 1999-11-29
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Mather, Jennie P.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L
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Hillan, Kenneth, J.
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maldi, Christopher J.
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ritsen, Mary E.
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P. Mickey
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f, Ellen
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APPLICANT: Usativey, remorth, J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Pan, James
APPLICANT: Roy, Margaret Ann
APPLICANT: Williams, Daniel
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US/09/665,350
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/2094
PRIOR APPLICATION NUMBER: PCT/US99/2094
PRIOR APPLICATION NUMBER: PCT/US99/2094
PRIOR APPLICATION NUMBER: PCT/US99/2094
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21090
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US-09-902-853-285
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Best Local S
Matches 53
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ANT: Ashkenazi, Avi
ANT: Botstein, David
ANT: Beenoyers, Luc
ANT: Eaton, Dan L.
ANT: Eston, Dan L.
ANT: Ferrara, Napoleone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 LTDEEKRLMVELHNLYRAQVSPT--ASDMLHMRWDEELAAFAKAYARQCVWGHNKERGRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 LDDDMREMFTELHNGYRAAFARNYKTSKMRTMVYDCTLEEKAYKSAEKC----SEEPSSE
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53; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQCP---SGYHC---- 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Grimaldi, Christopher J.
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Gerritsen, Mary E.
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Pred. No. 1.2e-07;
6; Mismatches 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72; Indels 34;
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US-09-907-824-285
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US-09-902-853-285
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PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR PILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/30991
PRIOR APPLICATION NUMBER: PCT/US99/30991
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
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SEQ ID NO 285
LENGTH: 463
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : Genentech, Inc.
Ashkenazi, Avi
: Botstein, David
: Desnoyers, Luc
: Eaton, Dan L.
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Similarity 28.6%; Pred. No. 1.2e-07;
53; Conservative 26; Mismatches 72; Indels 34;
                                                                                      Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
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Gerber, Hanspeter
Gerritsen, Mary E.
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Filvaroff, Ellen
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5. US20020197671A1
                                             javin, Ivar J.
ather, Jennie P.
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Nicholas F
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SEQ ID NO 285
LENGTH: 463
TYPE: PRT
ORGANITY
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US-09-907-824-285
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Best Local
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CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: 09/865,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PILING DATE: 1999-07-07
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APPLICATION NUMBER: US 60/146,222
APPLICATION 1999-07-28
TITING DATE: 1999-07-28
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FILING DATE: 1999-09-13
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                     193 KNSLC 197
                                                         174 QNLLC 178
                                                                                             140 IGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQCP---SGYHC---- 192
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53; Conservative
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                                                                                                                             LGCAVVDCS-----GKTHV----VCQYGPEAKGDGKTIYEEGAPCSRCSDYGAGVTCDDDW 173
                                                                                                                                                                 GENLFAITDEGMDVPL-AMEEWHHE-----REHYNLSAATCSPGQMCGHYTQVVWAKTER 139
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                                                                                                                                                                                                                                                                         LDDDMREMFTELHNGYRAAFARNYKTSKMRTMVYDCTLEEKAYKSAEKC----SEEPSSE 68
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Stewart, Timothy A.
Tumas, Daniel
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Pred. No. 1.
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1.2e-07;
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US-09-907-841-285

Sequence 285, Ap.

Publication No.

GENERAL INFORMAT
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US-09-907-841-285
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CURRENT FILING DATE: 2001-11-20
PRIOR FILING DATE: 2000-02-22
PRIOR PRIOR TILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: UT/US99/2054
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR PLING DATE: 1999-11-29
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NUMBER OF SEQ ID NOS:
SEQ ID NO 285
                                                                                                                                              Matches
69 EENVDVFSAATLNIPLEAGNSWWSEIFELRGKVYNKNGKTSNIANM ------VWDSHDK 121
                                              28
                                                                                            13 LDDDMREMFTELHNGYRAAFARNYKTSKMRTMVYDCTLEEKAYKSAEKC----SEEPSSE 68
                                                                                                                                                                                                                                                                                                                   463
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Williams, P. Mickey

Nood, William, I.

INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
INVENTION: Acids Encoding the Same
                                                                                                                                                                     Similarity
                                              LIDEEKRLMVELHNLYRAQVSPT--ASDMLHMRWDEELAAFAKAYARQCVWGHNKERGRR 85
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Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
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Hillan, Kenneth, J
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b. US20020198366A1
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                                                                                                                                           15.9%; Score 159; DE llarity 28.6%; Pred. No. 1.2e Conservative 26; Mismatches
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n1, Nicholas F.
, Margaret Ann
wart, Timothy A.
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Christopher J.
                                                                                                                                                                                                                                                                                                                                                                                         data removed -
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L.2e-07;
hes 72;
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                                                                                                                                                                                            Length 463;
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RESULT 14 US-09-904-011-285

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122 LGCAVVDCS-----GKTHV---VCQYGPEAKGDGKTIYEEGAPCSRCSDYGAGVTCDDDW 173
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
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Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
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Mather, Jennie P.
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Gao, Wei-Qiang
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Gerritsen, Mary E.
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5. US20030003530A1
                     NUMBER: PCT/US99/28564
1999-12-02
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FILE OF INVENTION:

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/028,072

CURRENT FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 60/049911.

PRIOR FILING DATE: 1997-06-18

PRIOR PEPLICATION NUMBER: 60/056974

PRIOR PEPLICATION NUMBER: 60/059113

PRIOR APPLICATION NUMBER: 60/059113

PRIOR FILING DATE: 1997-09-17

PRIOR PILING DATE: 1997-09-17

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PRIOR PILING DATE: 1997-09-17
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PRIOR FILING DATE: 1999-12-16
PRIOR PPILING DATE: 1999-12-16
PRIOR PPILING DATE: 1999-12-20
PRIOR PPILING DATE: 2000-01-05
SEQ ID NO 285
LENGTH: 463
SEQ ID NOS: 423
TYPE: PRE
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US-10-028-072-360
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US-09-904-011-285
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Publication No.
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53; Conservative
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Smith, Victoria
Stewart, Timothy A.
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Gerritsen, Mary E.
Goddard, Audrey
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Watanabe, Colin K
Wood, William
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o. US20030004311A1
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Llvaroff, Ellen
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TION NUMBER: 60/01 DATE: 1998-02-04 VION NUMBER: 60/01 VION NUMBER: 60/01 VION NUMBER: 60/01 DATE: 1998-03-20 DATE: 1998-03-20 DATE: 1998-03-20 DATE: 1998-03-20 DATE: 1998-03-20 DATE: 1998-03-27 VION NUMBER: 60/01 DATE: 1998-03-27 VION NUMBER: 60/01 DATE: 1998-03-27 VION NUMBER: 60/01 DATE: 1998-04-09 DATE: 1998-04-09 DATE: 1998-04-09 DATE: 1998-04-15 VION NUMBER: 60/01 DATE: 1998-04-16 VION NUMBER: 60/01 DATE: 1998-04-24 VION NUMBER: 60/01 DATE: 1998-04-29 DATE: 1998-04-29 VION NUMBER: 60/01 DATE: 1998-05-13 VION NUMBER: 60/01 DATE: 1998-06-10				
REPLICATION NUMBER: 60/01 FILING DATE: 1998-02-04 APPLICATION NUMBER: 60/01 APPLICATION NUMBER: 60/01 APPLICATION NUMBER: 60/01 FILING DATE: 1998-02-09 APPLICATION NUMBER: 60/01 FILING DATE: 1998-03-20 APPLICATION NUMBER: 60/01 FILING DATE: 1998-03-22 APPLICATION NUMBER: 60/01 FILING DATE: 1998-03-25 APPLICATION NUMBER: 60/01 FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/01 FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/01 FILING DATE: 1998-04-09 APPLICATION NUMBER: 60/01 FILING DATE: 1998-05-13 APPLICATION NUMBER: 60/01 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/06 FILING DATE: 1998-			************	************
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OR FILING DATE: 1997-09-17
OR APPLICATION NUMBER: 60/059122
OR FILING DATE: 1997-09-17
OR APPLICATION NUMBER: 60/059263
OR APPLICATION NUMBER: 60/059568
OR FILING DATE: 1997-09-19
OR APPLICATION NUMBER: 60/059568
OR FILING DATE: 1997-09-19
OR APPLICATION NUMBER: 60/06285
OR FILING DATE: 1997-09-19
OR APPLICATION NUMBER: 60/06286
OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/06286
OR FILING DATE: 1997-10-17
OR APPLICATION NUMBER: 60/062814
OR APPLICATION NUMBER: 60/063045
OR FILING DATE: 1997-10-24
OR APPLICATION NUMBER: 60/063045
OR APPLICATION NUMBER: 60/063020
OR APPLICATION NUMBER: 60/063020
OR APPLICATION NUMBER: 60/063327
OR APPLICATION NUMBER: 60/063735
OR FILLING DATE: 1997-10-29
OR APPLICATION NUMBER: 60/063735
OR FILLING DATE: 1997-10-29
OR APPLICATION NUMBER: 60/063735
OR FILLING DATE: 1997-11-12
OR APPLICATION NUMBER: 60/06424
OR APPLICATION NUMBER: 60/065186
OR APPLICATION NUMBER: 60/065186
OR APPLICATION NUMBER: 60/066511
OR APPLICATION NUMBER: 60/066912
OR APPLICATION NUMBER: 60/0669134

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RESULT 16
US-09-906-742-285
US-09-906-742-285
Sequence 285, Applicat
Publication No. US200
Publication No. TOOMARTION:
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PRIOR APPLICATION NUMBER: 60/089907
PRIOR APPLICATION NUMBER: 60/089947
PRIOR APPLICATION NUMBER: 60/089947
PRIOR APPLICATION NUMBER: 60/090349
PRIOR PELLING DATE: 1998-06-19
PRIOR PELLING DATE: 1998-06-29
PRIOR PELLING DATE: 1998-06-29
PRIOR PELLING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR APPLICATION NUMBER: 60/090445
PRIOR PILLING DATE: 1998-06-24
PRIOR PILLING DATE: 1998-06-24
PRIOR PILLING DATE: 1998-06-24
PRIOR PILLING DATE: 1998-06-26
PRIOR PILLING DATE: 1998-06-26
PRIOR PILLING DATE: 1998-06-26
PRIOR PILLING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091360
PRIOR APPLICATION NUMBER: 60/091519
PRIOR APPLICATION NUMBER: 60/091519
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILLING DATE: 1998-07-02
PRIOR FILLING DATE: 1998-07-02
PRIOR FILLING DATE: 1998-07-02
PRIOR FILLING DATE: 1998-07-02
PRIOR FILLING DATE: 1998-07-07
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1 Similarity 28.6%; Pred. No. 1.2e-07;
53; Conservative 26; Mismatches 72; Indels 34;
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Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Laton, Dan L.
                                                                                                                                                                                                                                                                                                                                         Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                             Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
                                           Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Godowski, Paul J.
Grimaldi, Christopher J.
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o. US20030023054A1
Williams, P. Mickey Wood, William, I.
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CURRENT FILLING DATE: 2002-07-20

PRIOR APPLICATION NUMBER: 07/65,350

PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 2000-09-22

PRIOR PELING DATE: 2000-09-22

PRIOR PELING DATE: 1999-07-26

PRIOR PELING DATE: 1999-07-26

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PRIOR PELING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR PELING DATE: 1999-07-28

PRIOR PELING DATE: 1999-09-08

PRIOR PELING DATE: 1999-09-13

PRIOR PELING DATE: 1999-09-13

PRIOR PELING DATE: 1999-09-15

PRIOR PELING DATE: 1999-09-15

PRIOR PELING DATE: 1999-10-15

PRIOR PELICATION NUMBER: PCT/US99/23089

PRIOR PELING DATE: 1999-10-05

PRIOR PELING DATE: 1999-11-20

PRIOR PELING DATE: 1999-11-20

PRIOR PELING DATE: 1999-11-20

PRIOR APPLICATION NUMBER: PCT/US99/28513

PRIOR PELING DATE: 1999-11-20

PRIOR PELING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/28565

PRIOR APPLICATION NUMBER: PCT/US99/28565

PRIOR PRIOR PELING DATE: 1999-12-02

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PRIOR PRIOR PRICING DATE: 1999-12-02

PRIOR PRICING PRICING NUMBER: PCT/US99/3099

PRIOR PRICING PRICING DATE: 1999-12-03

PRIOR PRICING PRICING NUMBER: PCT/US99/3099

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RESULT 17
US-10-121-049-360
; Sequence 360, Application US/10121049
; Publication No. US20030022239Al
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CURRENT APPLICATION NUMBER: US/09/906,742
CURRENT FILING DATE: 2001-07-16
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11 Similarity 28.6%;
53; Conservative
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; Pred. No. 1.2e-07;
26; Mismatches 72; Indels 34; Gaps
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RESULT 18
US-10-123-904-360
US-10-123-904-360
; Sequence 360, App.
; Publication No.
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CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 202-04-12
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 360
LENGTH: 463
TYPE: PRT
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US-10-121-049-360
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APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Mauro
APPLICANT: DeForge, Laura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 15.9%; Score 159; DB 9; Length 463; Best Local Similarity 28.6%; Pred. No. 1.2e-07; Matches 53; Conservative 26; Mismatches 72; Indels
                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 LDDDMREMFTELHNGYRAAFARNYKTSKMRTMVYDCTLEEKAYKSAEKC----SEEPSSE 68
                                                                            Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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Watanabe, Colin K
Wood, William
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Gurney, Austin L.
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Gerritsen, Mary E.
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DeForge, Laura
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                                     Tumas, Daniel
                                                          Stewart, Timothy A.
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b. US20030022328A1
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RESULT 19
US-10-140-470-360
; Sequence 360, Application US/10140470
; Publication No. US20030022331A1
; GENERAL INFORMATION:
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US-10-123-904-360
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Query Match 15.9
Best Local Similarity 28.6
Matches 53; Conservative
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 360
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 360
LENGTH: 463
TYPE: PRT
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CURRENT FILING DATE: 2002-04-16
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                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERENCE: P3330R1C160 CURRENT APPLICATION NUMBER: US/10/140,470 CURRENT FILING DATE: 2002-05-06
                                                                                                                                                       LENGTH: 463
TYPE: PRT
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Wood, William
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Gurney, Austin L.
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1larity 28.6%; Fred. No. 1.2e-07; Indels 34; Gaps
Conservative 26; Mismatches 72; Indels 34; Gaps
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15.9%; Score 159; DB 9; Length 463; 28.6%; Pred. No. 1.2e-07; ative 26; Mismatches 72; Indels

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FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/906,838

CURRENT ETLING DATE: 2001-07-16

PRIOR APPLICATION NUMBER: 09/655,350

PRIOR FILING DATE: 2000-09-18

PRIOR PLICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 2000-02-22

PRIOR PLICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 1999-07-05

PRIOR FILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR FILING DATE: 1999-07-26

PRIOR PRIOR PLICATION NUMBER: US 60/146,222

PRIOR PRIOR PLICATION NUMBER: PCT/US99/20594

PRIOR FILING DATE: 1999-09-18

PRIOR PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR PRIOR PLICATION NUMBER: PCT/US99/21090

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR APPLICATION NUMBER: PCT/US99/21547

PRIOR APPLICATION NUMBER: PCT/US99/23089

PRIOR APPLICATION NUMBER: PCT/US99/23089

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/23089

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/23089

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/23089

PRIOR FILING DATE: 1999-10-05
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US-09-906-838-285
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumms, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, Williams, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Tvar J.
Mather, Jennie P.
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Ashkenazi, Avi
Botstein, David
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Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
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PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28364
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/30991
PRIOR APPLICATION NUMBER: PCT/US99/30991
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 285
LENGTH: 463
TYPE: PRT
ORGANISM: Homo Sapien
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US-09-907-613-285
; Sequence 285, App
; Publication No. 1
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Best Local Sim
Matches 53;
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Similarity 28.6%; Pred. No. 1.2e-07;
53; Conservative 26; Mismatches 72; Indels 34; Gaps
                  Paoni, Nicholas F. Roy, Margaret Ann Stewart, Timothy A.
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Grimaldi, Christopher
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Gerber, Hanspeter
                                                                       Pan, James
Paoni, Nicholas F.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Ashkenazi, Avi
Botstein, David
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ther, Jennie P.
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PRIOR FILING DATE: 1999-12-20

PRIOR APPLICATION NUMBER: PCT/US99/30999

PRIOR FILING DATE: 2000-01-05

NUMBER OF SEQ ID NOS: 423

SEQ ID NO 285

LENGTH: 463

TYPE: PRT

ORGANISM: Homo Sapien

US-09-907-613-285
RESULT 22
US-09-907-942-285
; Sequence 285, Application US/09907942
; Publication No. US20030027146A1
; GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR P
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Best Local
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PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
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CURRENT APPLICATION NUMBER: US/09/907,613
CURRENT FILING DATE: 2001-07-17
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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FILING DATE: 1999-11-30
APPLICATION NUMBER: PCT/US99/28564
FILING DATE: 1999-12-02
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APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
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APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
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28.6%; Pre-
ative 26;
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Pred. No. 1.2e-07;
6; Mismatches 72;
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                                                                                                                                     : NUMBER OF SEQ ID NOS: 4:
; SEQ ID NO 285
; LENGTH: 463
; TYPE: PRT
; ORGANIZSM: Homo Saplen
US-09-907-942-285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 1046-14

CURRENT APPLICATION NUMBER: US/09/907,942

CURRENT APPLICATION NUMBER: US/09/907,942

CURRENT APPLICATION NUMBER: US/09/907,942

PRIOR APPLICATION NUMBER: US/09/004414

PRIOR APPLICATION NUMBER: US/09/004414

PRIOR FILLING DATE: 1999-07-07

PRIOR FILLING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US/09/145,698

PRIOR APPLICATION NUMBER: US/01/45,698

PRIOR APPLICATION NUMBER: US/01/45,698
     Query Match
Best Local Similarity
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PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
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PRIOR APPLICATION NUMBER: PU
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PRIOR APPLICATION NUMBER: PU
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DR APPLICATION WIMBER: PCT/OR APPLICATION WIMBER
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Ashkenazi, Avi
: Botstein, David
: Desnoyers, Luc
: Eaton, Dan L.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
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Hillan, Kenneth, J.
Kljavin, Ivar J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Godowski, Paul J.
Grimaldi, Christopher J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gerber, Hanspeter
Gerritsen, Mary E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1lvaroff,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      od, William,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ther, Jennie P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         We1-Qiang
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f, Ellen
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          Score 159; DB 9;
Pred. No. 1.2e-07;
                                                     Length 463;
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; ORGANISM: Homo Sapien
US-10-175-746-360
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Best Local S
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: DeForge, Laura
APPLICANT: Deforgers, Luc
APPLICANT: Filwaroff, Ellen
APPLICANT: Gao, Wel-Olang
APPLICANT: Goodwal-Olang
APPLICANT: Goddward, Mary E.
APPLICANT: Goddward, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
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CURRENT FILING DATE: 2002-06-19
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C353
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                                                                                           140 IGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQCP---SGYHC---- 192
193 KNSLC 197
                                               174 QNLLC 178
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                                                                                                                                        122 LGCAVVDCS-----GKTHV---VCQYGPEAKGDGKTIYEEGAPCSRCSDYGAGVTCDDDW 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 QNLLC 178
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                                                                                                                                                                                                                                                                                                                                   13 LDDDMREMFTELHNGYRAAFARNYKTSKMRTMYYDCTLEEKAYKSAEKC----SEEPSSE 68
                                                                                                                                                                                             86 GENLFAITDEGMDVPL-AMEEWHHE-----REHYNLSAATCSPGQMCGHYTQVVWAKTER 139
                                                                                                                                                                                                                                             69 EENVDVFSAATLNIPLEAGNSWWSEIFELRGKVYNKNGKTSNIANM------VWDSHDK 121
                                                                                                                                                                                                                                                                                               28 LTDEEKRLMVELHNLYRAQVSPT--ASDMLHMRWDEELAAFAKAYARQCVWGHNKERGRR 85
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                                                                                                                                                                                                                                                                                                                                                                                              h 15.9%; Score 159; DB 9; Length 463;
Similarity 28.6%; Pred. No. 1.2e-07;
53; Conservative 26; Mismatches 72; Indels 34; Gaps
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FILE REFERENCE: P3330R1C382
CURRENT APPLICATION NUMBER: US/10/176,918
CURRENT FILING DATE: 2002-06-20
PRIOT APPLICATION Encoved - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
LENGTH: 463
TYPE: PRT
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US-10-176-918-360
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Best Local S
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                                                                                                                                              APPLICANT:
                                                                                                                                                                                          APPLICANT: Baker, Kevin P. APPLICANT: Beresini, Maur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 15.9%; Score 159; DB 9; Length 463; Local Similarity 28.6%; Pred. No. 1.2e-07; Indels 34; Gaps 53; Conservative 26; Mismatches 72; Indels 34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         193 KNSLC 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 EENVDVFSAATLNIPLEAGNSWWSEIFELRGKVYNKNGKTSNIANM-----VWDSHDK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 LDDDMREMFTELHNGYRAAFARNYKTSKMRTMVYDCTLEEKAYKSAEKC----SEEPSSE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 LTDEEKRLMVELHNLYRAQVSPT--ASDMLHMRWDEELAAFAKAYARQCVWGHNKERGRR 85
           Goddard, Audrey
Godowski, Paul
                                                                                                             Desnoyers, Luc
Filvaroff, Ellen
                                                                                                                                                                   Beresini, Maureen
DeForge, Laura
                                                                 Gerritsen, Mary E.
                                                                                        Gao, We1-Q1ang
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                                                                                                                                                                                                                                                                    Application US/10176921
o. US20030027276A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/10176918
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RESULT 26
US-10-137-865-360
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US-10-176-921-360
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APPLICANT: Beresini Maureen
APPLICANT: Beresini Maureen
APPLICANT: Desnoyers Luc
APPLICANT: Filvaroff Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Geritsen, Mary E.
APPLICANT: Godowski, Paul J.
APPLICANT: Gudowski, Paul J.
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood Steven
APPLICANT: Smith, Victoria
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330NELIGS4 CURRENT APPLICATION NUMBER: US/10/137,865 CURRENT EILING DATE: 2002-05-03 Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550 SEQ ID NOS: 550 ID N
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APPLICANT: Watanabe, Colin K
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P330R1C288
CURRENT FILING DATE: 2002-06-20
CURRENT APPLICATION NUMBER: US/10/176,921
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Publication No. US2
GENERAL INFORMATION
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Best Local
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APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 EENVDVFSAATLNIPLEAGNSWWSEIFELRGKVYNKNGKTSNIANM------VWDSHDK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 GENLFAITDEGMDVPL-AMEEWHHE-----REHYNLSAATCSPGOMCGHYTOVVWAKTER
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D. US20030032155A1
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US-10-140-474-360
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US-10-140-474-360
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US-10-137-865-360
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P339081C162
CURRENT APPLICATION NUMBER: US/10/140,474
CURRENT EPILING DATE: 2002-05-06
PTIOT APPLICATION TEMPORED - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 360
LENGTH: 463
TYPE: PRT
                                                                                                                                                                                                                                                                          Ouery Match 15.9%; Score 159; DB 9; Length 463; Best Local Similarity 28.6%; Pred. No. 1.2e-07; Matches 53; Conservative 26; Mismatches 72; Indels 34;
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Best Local
122 LGCAVVDCS-----GKTHV---VCQYGPEAKGDGKTIYEEGAPCSRCSDYGAGVTCDDDW 173
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                                                                         86 GENLFAITDEGMDVPL-AMEEWHHE-----REHYNLSAATCSPGQMCGHYTQVVWAKTER 139
                                                                                                                          69 EENVDVFSAATLNIPLEAGNSWWSEIFELRGKVYNKNGKTSNIANM------VWDSHDK 121
                                                                                                                                                                         28 LTDEEKRLMVELHNLYRAQVSPT--ASDMLHMRWDEELAAFAKAYARQCVWGHNKERGRR 85
                                                                                                                                                                                                                        13 LDDDMREMFTELHNGYRAAFARNYKTSKMRTMYYDCTLEEKAYKSAEKC----SEEPSSE 68
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Similarity 28.6%; Pred. No. 1.2e-07;
53; Conservative 26; Mismatches 72;
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Watanabe, Colin K
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5. US20030032156A1
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RESULT 28
US-09-904-820-285
; Sequence 285, Ap;
; Publication No.;
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PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR APPLICATION NUMBER: PCT/US99/30911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
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                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US99/28313 FILING DATE: 1999-11-30
                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US99/28214 FILING DATE: 1999-11-29
                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT FILING DATE: 1999-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US99/21090 FILING DATE: 1999-09-15
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US99/21547
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Ashkenazi, Avi
Botstein, David
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Stewart, Timothy A.
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Hillan, Kenneth, J.
Kijavin, Ivar J.
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Grimaldi, Christopher J.
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Eaton, Dan L.
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o. US20030036094A1
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: SEQ ID NO 285
: LENGTH: 463
: TYPE: PRT
: ORGANISM: Homo Sapien
US-09-904-820-285
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US-09-904-859-285
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Best Local (
                    APPLICANT: Tumas, Daniel APPLICANT: Williams, P. Mickey APPLICANT: Williams, P. Mickey APPLICANT: Williams, P. Mickey APPLICANT: Wood, William, I. TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14 CURRENT PLICATION NUMBER: US/09/904,859 CURRENT PILING DATE: 2001-07-12 PRIOR APPLICATION NUMBER: 09/665,350 PRIOR APPLICATION NUMBER: 09/665,350 PRIOR FILING DATE: 2000-09-18 PRIOR FILING DATE: 2000-09-22 PRIOR FILING DATE: 2000-02-22 Current PRIOR FILING DATE: 2000-02-22 Cu
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PRIOR APPLICATION UNMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION UNMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
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                                                                                                                                                                                                                                                                                                                                                                           Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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Ashkenazi, Avi
Botstein, David
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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o. US20030036060A1
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A.
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f, Ellen
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Christopher J.
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RESULT 30
US-09-909-204-285
: Sequence 285, Application US/09909204
: publication No. US20030036061A1
; GENERAL INFORMATION:
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US-09-904-859-285
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PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-20
PRIOR PRIOR PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR POPONO NUMBER: PCT/US99/30999
PRIOR FILING DATE: 2000-01-05
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Best Local S
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NUMBER OF SEQ ID NOS: 423
SEQ ID NO 285
LENGTH: 463
TYPE: PRT
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                                                                                     APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
     APPLICANT:
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RIOR APPLICATION NUMBER: US 60/145,698
RIOR FILING DATE: 1999-07-26
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FILING DATE: 1999-10-05
APPLICATION NUMBER: PCT,
FILING DATE: 1999-11-29
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FILING DATE: 1999-09-13
APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
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FILING DATE: 1999-11-30
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FILING DATE: 1999-09-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 GENLFAITDEGMDVPL-AMEEWHHE-----REHYNLSAATCSPGQMCGHYTQVVWAKTER 139
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Fong, Sherman
Gao, Wei-Qiang
                                            Filvaroff,
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                                            , Napoleone
ff, Ellen
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28.6%; Pred. No. 1.2e-07;
ative 26; Mismatches 72; Indels 34; Gaps
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PRILE REFERENCE: 1040b-14
CURRENT APPLICATION NUMBER: US/09/909,204
CURRENT PILLING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: DCT/US00/04414
PRIOR PRIOR PILLING DATE: 2000-02-22
PRIOR PRIOR PILLING DATE: 2000-02-23
PRIOR PILLING DATE: 2000-02-26
PRIOR PRILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILLING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PILLING DATE: 1999-09-08
PRIOR PILLING DATE: 1999-09-08
PRIOR PILLING DATE: 1999-09-18
PRIOR PILLING DATE: 1999-09-18
PRIOR PILLING DATE: 1999-09-18
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR PILLING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR PILLING DATE: 1999-10-05
PRIOR PILLING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PILLING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PILLING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PILING DATE: 1999-12-20
PRIOR PRIOR PILING DATE: 1999-12-20
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US-09-909-204-285
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Best Local S
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PPLICANT: Wood, William, I.
ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITLE OF INVENTION: Acids Encoding the Same
86 GENLFAITDEGMDVPL-AMEEWHHE-----REHYNLSAATCSPGONCGHYTQVVWAKTER 139
                                                                                                                                                                                                                13 LDDDMREMFTELHNGYRAAFARNYKTSKMRTMYYDCTLEEKAYKSAEKC----SEEPSSE 68
                                                                    69 EENVDVFSAATLNIPLEAGNSWWSEIFELRGKVYNKNGKTSNIANM ----- VWDSHDK 121
                                                                                                                                            28 LTDEEKRLMVELHNLYRAQVSPT--ASDMLHMRWDEELAAFAKAYARQCVWGHNKERGRR 85
                                                                                                                                                                                                                                                                                         53;
                                                                                                                                                                                                                                                                                         Similarity 28.6
53; Conservative
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Stewart, Timothy A.
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Mather, Jennie P.
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Hillan, Kenneth, J.
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28.68; Pred. No. 1.2e-07;
tive 26; Mismatches 72; Indels 34; Gaps
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RESULT 32
US-10-143-114-360
Sequence 360, Application US/10143114
Publication No. US20030036180A1
GENERAL INFORMATION:
APPLICANT: Baker Kevin P.
APPLICANT: Beresini, Maureen
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US-10-142-431-360
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US-10-142-431-360
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Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
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LENGTH: 463
TYPE: PRI
ORGANYON
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RRENT APPLICATION UMBER: US/10/142,431
RRENT FILING DATE: 2002-05-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 28.6
53; Conservative
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Desnoyers, Luc
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0. US20030036179A1
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                                                                                                                                                                                                                                                                                                                                Sequence 20., Sequence 20., Publication No. US200., Publication INFORMATION:
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; ORGANISM: Homo Sapien
US-10-143-114-360
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APPLICANT:
APPLICANT:
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Best Local
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TILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 15.9%; Score 159;
Local Similarity 28.6%; Pred. No. 1.
es 53; Conservative 26; Mismatche
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                                                                                                                                                                                                            Genentech, Inc.
Ashkenazi, avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Shorman
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
                                                                                                                              Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
    Kljavin, iva-
Kljavin, iva-
--her, Jennie P.
                                                                                         Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
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Wood, William
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Filvaroff, Ellen
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                                     Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
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                                                                                                                                                                                                          Sherman
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Matches

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RESULT 34
US-09-906-646-285
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; Publication No.
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US-09-904-786-285
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CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 265
LENGTH: 463
TYPE: PRT
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Best Local :
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ILE REFERENCE: 10466-14
                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 LDDDMREMFTELHNGYRAAFARNYKTSKMRTMVYDCTLEEKAYKSAEKC----SEEPSSE 68
F: Wood, William, I.
INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
INVENTION: Acids Encoding the Same
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53; Conservative
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Roy, Margaret Ann
Stewart, Timothy A.
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Goddard, A.
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                                                                                       Stewart,
                                                                    Tumas, Daniel
                                                                                                                                                             Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
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                                     ood, William, I.
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iton, Dan L.
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                                                                                 Margaret Ann wart, Timothy A.
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                                                                                                                                                 Jennie P.
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f, Ellen
                                                                                                                                                                                                                  Christopher J.
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28.6%;
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Pred. No. 1
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PRIOR APPLICATION NUMBER: E PRIOR FILING DATE: 2000-01; NUMBER OF SEQ ID NOS: 423 SEQ ID NO 285 LENGTH: 463 LENGTH: 463 TYPE: PRT ORGANISM: Homo Sapien US-09-906-646-285
                                                                                                     RESULT 35
US-09-906-700-285
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CURRENT APPLICATION NUMBER: US/09/906,646
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
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PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28565
Sequence 285, Applic Publication No. US20 GENERAL INFORMATION:
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Best Local
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RIOR APPLICATION NUMBER: PCT/US99/30095
RIOR FILING DATE: 1999-12-16
RIOR APPLICATION NUMBER: PCT/US99/30911
RIOR FILING DATE: 1999-12-20
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                                                                                                                                                                                                                                                                                                         174 QNLLC 178
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                                                                                                                                                                                                                                                                                                                                                                                                              122 LGCAVVDCS-----GKTHV----VCQYGPEAKGDGKTIYEEGAPCSRCSDYGAGVTCDDDW 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 EENVDVFSAATLNIPLEAGNSWWSEIFELRGKVYNKNGKTSNIANM-----VWDSHDK 121
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l Similarity 28.6%;
53; Conservative 2
                                       Application US/09906700 p. US20030039972A1
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Pred. No. 1.2e-07;
6; Mismatches 72;
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APPLICANT: APPLICANT: APPLICANT:

Genentech, Inc. Ashkenazi, Avi Botstein, David

Desnoyers, Eaton, Dan

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PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US09/00219
PRIOR FILING DATE: 2000-001-05
PRIOR FILING DATE: 2000-001-05
INUMBER OF SEQ ID NOS: 423
SEQ ID NO 285
LENGTH: 463
TYPE: PRT
ORGANISM: Homo Sapien
US-09-906-700-285
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/906,700

CURRENT FILING DATE: 2000-09-18

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR APPLICATION NUMBER: US 60/145,22

PRIOR FILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR APPLICATION NUMBER: PCT/US99/20944

PRIOR APPLICATION NUMBER: PCT/US99/20944

PRIOR APPLICATION NUMBER: PCT/US99/2094

PRIOR APPLICATION NUMBER: PCT/US99/2094

PRIOR APPLICATION NUMBER: PCT/US99/2099

PRIOR APPLICATION NUMBER: PCT/US99/23089

PRIOR APPLICATION NUMBER: PCT/US99/28514

PRIOR APPLICATION NUMBER: PCT/US99/28544

PRIOR APPLICATION NUMBER: PCT/US99/28544

PRIOR APPLICATION NUMBER: PCT/US99/28544

PRIOR APPLICATION NUMBER: PCT/US99/28564

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13 LDDDMREMFTELHNGYRAAFARNYKTSKMRTMVYDCTLEEKAYKSAEKC----SEEPSSE 68
                                                               Similarity 28.6
53; Conservative
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***her, Jennie P.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Grimaldi, Christopher J.
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Stewart, Timothy A.
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Filvaroff, Ellen
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RESULT 37
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TITLE OF INVENTION: SECRETED AND TRANSHEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C59
CURRENT ENTING DATE: 2007-05-06
CURRENT ENTLING DATE: 2007-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 360
LENGTH: 463
TYPES: 07-05-06
DENGTH: 463
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Best Local S
Matches 53
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
The Start Wood, William
The Start Wood, William
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                                                            193 KNSLC 197
                                                                                                  174 QNLLC 178
                                                                                                                                           140 IGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQCP---SGYHC----
                                                                                                                                                                      122 LGCAVVDCS-----GKTHV----VCQYGPEAKGDGKTIYEEGAPCSRCSDYGAGVTCDDDW 173
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                                                                                                                                                                                                                                                             69 EENVDVFSAATLNIPLEAGNSWWSEIFELRGKVYNKNGKTSNIANM------VWDSHDK 121
                                                                                                                                                                                                                                                                                                                                     13 LDDDMREMFTELHNGYRAAFARNYKTSKMRTMVYDCTLEEKAYKSAEKC----SEEPSSE 68
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Gurney, Austin L.
Sherwood, Steven
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Gerritsen, Mary E.
Goddard, Audrey
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DeForge, Laura
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5. US20030037623A1
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                                                                                                                                                                                                                                                                                                                                                                                     15.9%; Score 159; DB 9; Length 463; 28.6%; Pred. No. 1.2e-07; tive 26; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                        Indels 34;
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DB 9; L l.2e-07; hes 72;

Length 463; Indels 34;

Gaps

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FILE REPERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/902,903

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR APPLICATION NUMBER: PCT/US99/20944

PRIOR APPLICATION NUMBER: PCT/US99/20944

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR APPLICATION NUMBER: PCT/US99/21547

PRIOR APPLICATION NUMBER: PCT/US99/21547
                                                 NUMBER OF SEQ ID NOS:
SEQ ID NO 285
LENGTH: 463
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Sequence 285, Ap
Publication No.
                                                                                                                         PRIOR APPLICATION NUMBER: PCT PRIOR FILING DATE: 2000-01-05
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPLICANT: Tumas, Daniel
PPLICANT: Williams, P. Mickey
PPLICANT: Wood, William, I.
TILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITLE OF INVENTION: Acids Encoding the Same
ILE REFERENCE: 10466-14
                                                                                                                                                                                                                     NR APPLICATION NUMBER: PCT/OR FILING DATE: 1999-12-02
OR APPLICATION NUMBER: PCT/OR APPLICATION NUMBER: PCT/OR FILING DATE: 1999-12-16
OR FILING DATE: 1999-12-20
OR FILING DATE: 1999-12-20
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NE FILING DATE: 1999-10-05

PR APPLICATION NUMBER: PCT

PR FILING DATE: 1999-12-02
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Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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Hillan, Kenneth, J.
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Grimaldi, Christopher J.
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Filvaroff, Ellen
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Gerritsen, Mary E.
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D. US20030044839A1
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US-09-903-749A-285
(Sequence 285, Application US/09903749A
Publication No. US20030045693A1
GENERAL INFORMATION:
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                                                                  PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 1000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR PPLICATION NUMBER: PCT/US99/2054
PRIOR PILING DATE: 1999-09-18
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/903,749A
CURRENT FILING DATE: 2001-07-11
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Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
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Wood, William,
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Ashkenazi, Avi
Botstein, David
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""+her, Jennie P
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vart, Timothy A.
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NUMBER: PCT/US99/21547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Snerman
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                            999-09-
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                                                 PCT/US99/21090
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PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR ELIUNG DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PILING DATE: 1999-11-29
PRIOR PELICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/30991
PRIOR APPLICATION NUMBER: PCT/US99/30991
PRIOR APPLICATION NUMBER: PCT/US99/30991
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-13-20
PRIOR PILING DATE: 1999-13-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-13-20
PRIOR POSSON NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-13-20
PRIOR PILING DATE: 1999-13-20
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US-09-903-749A-285
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US-09-903-786-285
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Best Local S
Matches 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION
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Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
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53; Conservative
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                                                                                                              Fong, Sherman
Gao; Wei-Qiang
Garber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
Goddwski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kijavin, Tvar J.
Kijavin, Tvar J.
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                                                                    Kljavin, Iva.
Kljavin, Iva.
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b. US20030044793A1
Pan, James
Paoni, Nicholas F
Roy, Margaret Ann
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PATITLE OF INVENTION: Acids Encoding the Same
FILLE OF INVENTION: Acids Encoding the Same
FILLE OF INVENTION: Acids Encoding the Same
FILLE OF INVENTION: Acids Encoding the Same
FULLE COUREST STILING DATE: 2001-07-11
CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: 02/05-09-18
PRIOR PAPLICATION NUMBER: 02/05-09-18
PRIOR PELLING DATE: 1999-07-07
PRIOR PELLING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-07
PRIOR PELLING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PELLING DATE: 1999-07-08
PRIOR PELLING DATE: 1999-07-08
PRIOR PELLING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR PELLING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR APPLICATION NUMBER: PCT/US99/23013
PRIOR PILING DATE: 1999-11-25
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/28564
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Best Local S
Matches 53
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PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 285
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193 KNSLC 197
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                                                                                                                                                                                                                                                                                                                                  86
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53; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.6%;
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; Pred. No. 1.2e-07;
26; Mismatches 72; Indels 34;
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US-10-142-419-360
US-10-142-419-360
; Sequence 360, Applica
; Publication No. US200
; GENERAL INFORMATION:

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; ORGANISM: Homo Sapien
US-10-142-419-360
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 360
LENGTH: 463
                                                                                                                                                                                                                                                                                                                                    Sequence 285, Application US/09902736 Publication No. US20030049676A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                              APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/142,419
CURRENT FILING DATE: 2002-05-10
Prior Apploication removed - See File Wrapper or Palm
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APPLICANT: Beresini, Maure
APPLICANT: DeForge, Laura
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 IGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQCP---SGYHC---- 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 GENLFAITDEGMDVPL-AMEEWHHE-----REHYNLSAATCSPGQMCGHYTQVVWAKTER 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 EENVDVFSAATLNIPLEAGNSWWSEIFELRGKVYNKNGKTSNIANM------VWDSHDK 121
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                                                                                                                                Desnoyers, Luc
Eaton, Dan L
Ferrara, Napoleone
Filvaroff, Ellen
                                                                        Gao, Wel-Qlang
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Smith, Victoria
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Goddard, A.
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Filvaroff, Ellen
                       Gerber, Hanspeter
Gerritsen, Mary E
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DS20030044945A1
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28.6%; Pred. No. 1.2e-07; Indels 34; Gaps
ative 26; Mismatches 72; Indels 34; Gaps
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PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR PILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30991
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PILING DATE: 1999-12-20
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PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR PLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-08
PRIOR PRICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
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NUMBER OF SEQ ID NOS: 423
SEQ ID NO 285
LENGTH: 463
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PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/C
PRIOR PILING DATE: 1999-09-15
PRIOR APPLICATION UNUMBER: PCT/C
PRIOR FILING DATE: 1999-10-05
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CURRENT FILING DATE: 2001-07-10
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                                                                                                                                                                                         13 LDDDMREMFTELHNGYRAAFARNYKTSKMRTMVYDCTLEEKAYKSAEKC----SEEPSSE 68
                                                                                                                                    28 LTDEEKRLMVELHNLYRAQVSPT--ASDMLHMRWDEELAAFAKAYARQCVWGHNKERGRR 85
                       86 GENLFAITDEGMDVPL-AMEEWHHE-----REHYNLSAATCSPGOMCGHYTOVVWAKTER 139
                                                                               69 EENVDVFSAATLNIPLEAGNSWWSEIFELRGKVYNKNGKTSNIANM-----VWDSHDK 121
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Grimaldi, Christopher J.
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Mather, Jennie P.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Wart, Timothy A.
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Query Match Best Local S Matches

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TYPE: PRT

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RESULT 41 US-09-902-736-285

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APPLICANT: Pan, James
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,119
CURRENT APPLICATION NUMBER: US/09/904,119
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US/09/904,119
CURRENT APPLICATION NUMBER: US/09/904,119
PRIOR APPLICATION NUMBER: US/01/43,048
PRIOR APPLICATION NUMBER: PCT/US99/2054
PRIOR APPLICATION NUMBER: PCT/US99/2054
PRIOR APPLICATION NUMBER: PCT/US99/2054
PRIOR APPLICATION NUMBER: US/01/53/2089
PRIOR APPLICATION NUMBER: US/01/53/2089
PRIOR APPLICATION NUMBER: US/01/53/2089
PRIOR APPLICATION NUMBER: PCT/US99/2054
PRIOR APPLICATION NUMBER: PCT/US99/2056
PRIOR APPLICATION NUMBER: PCT/US99/2056
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PRIOR APPLICATION NUMBER: PCT/US99/2056
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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Grimaldi, Christopher
Gurney, Austin L.
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Gerritsen, Mary E.
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                                                                        ON NUMBER: PCT/US99/28565
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PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR TILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 285
LENGTH: 463
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US-09-904-119-285
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
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Matches 53
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APPLICANT: Pach, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timchby A.
APPLICANT: Stewart, Timchby A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
APPLICANTON NUMBER: US/09/904,956
CURRENT PILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: ECT/US00/04414
PRIOR APPLICATION NUMBER: US/09/904,956
PRIOR APPLICATION NUMBER: US/09/904,956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 LDDDMREMFTELHNGYRAAFARNYKTSKMRTMVYDCTLEEKAYKSAEKC----SEEPSSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86 GENLFAITDEGMDVPL-AMEEWHHE-----REHYNLSAATCSPGOMCGHYTOVVWAKTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 EENVDVFSAATLNIPLEAGNSWWSEIFELRGKVYNKNGKTSNIANM------VWDSHDK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.9%; Score 159; DB 9; Length 463; Similarity 28.6%; Pred, No. 1 2e-07; E-07; Standardres 72; Indels
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Mather, Jennie P.
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Godowski, Paul J.
Grimaldi, Christopher J.
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DS20030049622A1
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FILING DATE: 1999-0/-0/
APPLICATION NUMBER: US 60/145,698
FILING DATE: 1999-07-26
FILING DATE: 1999-07-26
FILING DATE: 1999-07-26

US 60/146,222

FILING DATE: 1999-09-13
APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15 APPLICATION NUMBER: PCT/US99/20944 FILING DATE: 1999-09-13 APPLICATION NUMBER: PCT/US99/20594 FILING DATE: 1999-09-08

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140 IGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQCP---SGYHC---- 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86 GENLFAITDEGMDVPL-AMEEWHHE-----REHYNLSAATCSPGOMCGHYTQVVWAKTER 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 LDDDMREMFTELHNGYRAAFARNYKTSKMRTMVYDCTLEEKAYKSAEKC----SEEPSSE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EENVDVFSAATLNIPLEAGNSWWSEIFELRGKVYNKNGKTSNIANM-----VWDSHDK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGCAVVDCS-----GKTHV----VCQYGPEAKGDGKTIYEEGAPCSRCSDYGAGVTCDDDW 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIDEEKRLMVELHNLYRAQVSPT--ASDMLHMRWDEELAAFAKAYARQCVWGHNKERGRR 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 159; DB 9; Length 463;
; Pred. No. 1.2e-07;
26; Mismatches 72; Indels 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Secreted and Transmembrai TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/99/907,794

CURRENT APPLICATION NUMBER: 09/65.350

PRIOR APPLICATION NUMBER: 09/65.350

PRIOR FILLING DATE: 2000-09-18

PRIOR PRILING DATE: 2000-09-22

PRIOR PRILING DATE: 1999-07-07

PRIOR PRILING DATE: 1999-07-07

PRIOR PRILING DATE: 1999-07-08

PRIOR PRILING DATE: 1999-07-08

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR APPLICATION NUMBER: PCT/US99/2054

PRIOR APPLICATION NUMBER: PCT/US99/2094

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR APPLICATION NUMBER: PCT/US99/21547

PRIOR APPLICATION NUMBER: PCT/US99/21547

PRIOR APPLICATION NUMBER: PCT/US99/21547

PRIOR APPLICATION NUMBER: PCT/US99/21547

PRIOR APPLICATION NUMBER: PCT/US99/28313

PRIOR APPLICATION NUMBER: PCT/US99/28313

PRIOR APPLICATION NUMBER: PCT/US99/28313

PRIOR APPLICATION NUMBER: PCT/US99/28564

PRIOR FILLING DATE: 1999-11-30

PRIOR APPLICATION NUMBER: PCT/US99/28564

PRIOR APPLICATION NUMBER: PCT/US99/28565

PRIOR APPLICATION NUMBER: PCT/US99/28565

PRIOR APPLICATION NUMBER: PCT/US99/28565

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PRIOR APPLICATION NUMBER: PCT/US99/30999

PRIOR APPLICATION NUMBER: PCT/US99/30999
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                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT; ORGANISM: Homo Sapien US-09-907-794-285
                                                                                                                                                                                               Query Match
Best Local S:
Matches 53
                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
SEQ ID NO 285
LENGTH: 463
                                                                                                                                 13 LDDDMREMFTELHNGYRAAFARNYKTSKMRTWYYDCTLEEKAYKSAEKC----SEEPSSE
                                                                  28 LTDEEKRLMVELHNLYRAQVSPT---ASDMLHMRWDEELAAFAKAYARQCVWGHNKERGRR 85
                                                                                                                                                                                               ch 15.9%; Score 159; DB 9; 1
1 Similarity 28.6%; Pred. No. 1.2e-07;
53; Conservative 26; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INVENTION: Secreted and Transmembrane Polypeptides and Nucleic INVENTION: Acids Encoding the Same
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Paoni, Nicholas F.
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Stewart, Timothy A.
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Grimaldi, Christopher
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P. Mickey
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                                                                                                                                                                                                                                                          Length 463;
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PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
I NUMBER OF SEQ ID NOS: 423
SEQ ID NO 285
LENGTH: 463
TYPE: PRT
ORGANISM: Homo Sapien
US-09-904-956-285

PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20

APPLICATION NUMBER: PCT/US99/28565
FILING DATE: 1999:12-07
APPLICATION NUMBER: PCT/US99/30095
FILING DATE: 1999:12-16
APPLICATION NUMBER: PCT/US99/30911
FILING DATE: 1999:12-20

APPLICATION NUMBER: PCT/US99/28564 FILING DATE: 1999-12-02

APPLICATION NUMBER: PCT/US99/28313 FILING DATE: 1999-11-30

APPLICATION NUMBER: PCT/US99/28214 FILING DATE: 1999-11-29

APPLICATION NUMBER: PCT FILING DATE: 1999-10-05 APPLICATION NUMBER: POFILING DATE: 1999-09-

PCT/US99/23089 PCT/US99/21547

gs-

-09-907-794-285 Sequence 285, A

RAL INFORMATION:

Application US/09907794 o. US20030049677A1

Genentech, Inc.
Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.

Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang

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69

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Query Match Best Local S Matches 53

ch 15.9%; 1 Similarity 28.6%; 53; Conservative 26

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RESULT 45
US-10-123-262-360
; Sequence 360, App
; Publication No. 1
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CURRENT APPLICATION NUMBER: U5/10/123,262
CURRENT FILING DATE: 2002-04-15
PRIOT Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 360
LENGTH: 463
TYPE: PRI
ORGANISM: Homo Sapien
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Search completed: July 15, 2003, 08:37:15 Job time: 26 secs
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                                                                           193 KNSLC 197
                                                                                                           174 QNLLC 178
                                                                                                                                                        140 IGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQCP---SGYHC---- 192
                                                                                                                                                                                           122 LGCAVVDCS-----GKTHV----VCQYGPEAKGDGKTIYEEGAPCSRCSDYGAGVTCDDDW 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
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                                                                                                                                                                                                                                                                                                                                        13 LDDDMREMFTELHNGYRAAFARNYKTSKMRTMVYDCTLEEKAYKSAEKC----SEEPSSE 68
                                                                                                                                                                                                                                   86 GENLFAITDEGMDVPL-AMEEWHHE-----REHYNLSAATCSPGQMCGHYTQVVWAKTER 139
                                                                                                                                                                                                                                                                         69 EENVDVFSAATLNIPLEAGNSWWSEIFELRGKVYNKNGKTSNIANM------VWDSHDK 121
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Geddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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o. US20030049816A1
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eresini,Maureen
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Result
No.
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Gapop 10.0 , Gapext 0.5
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1 EGDYSLCQQREKLDDDMREM......DYGAGVTCDDDWQNLLCIGH 181
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Copyright (c) 1993 - 2003 Compugen Ltd.
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ALIGNMENTS

RESULT 2 1724493 hypothetical protein T05A10.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000 C;Accession: T24493 R;Sulatton, J. submitted to the EMBL Data Library, November 1995 A;Reference number: 219898 A;Accession: T24493 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-246 <wild- a;cross-references:="" a;experimental="" cesp:t05a10.5="" clone="" embl:268108;="" gspdb:gn00028;="" pidn:caa92136.1;="" source:="" t05a10<="" th=""><th>Qy 143 AKGDGKTIYEEGAPCSRCSDY 163 : : : : Db 214 NKTEGOPIYKVGTPCDDCSEY 234</th><th>99 154 143 214</th><th>Qy 51 EERAYKSAEKCSBEPSSEEENVDV </th><th>Qy 14 DDDMREWFTELHNGYRAAFARNYDD 15 NDSIRLQFLAWHNGYRSKLALGHISITEESESDDDD</th><th>Query Match 29.1%; Score 290; DB 2; Length 274 Best Local Similarity 34.3%; Pred. No. 1.7e-18; Matches 69; Conservative 23; Mismatches 57; Indels</th><th>A;Residues: 1-274 <moy> A;Cross-references: GB:L27427; NID:g440279; PIDN:AAA27789.1; PID:g440280</moy></th></wild->	Qy 143 AKGDGKTIYEEGAPCSRCSDY 163 : : : : Db 214 NKTEGOPIYKVGTPCDDCSEY 234	99 154 143 214	Qy 51 EERAYKSAEKCSBEPSSEEENVDV	Qy 14 DDDMREWFTELHNGYRAAFARNYDD 15 NDSIRLQFLAWHNGYRSKLALGHISITEESESDDDD	Query Match 29.1%; Score 290; DB 2; Length 274 Best Local Similarity 34.3%; Pred. No. 1.7e-18; Matches 69; Conservative 23; Mismatches 57; Indels	A;Residues: 1-274 <moy> A;Cross-references: GB:L27427; NID:g440279; PIDN:AAA27789.1; PID:g440280</moy>
<pre>iitis elegans Oct-1999 #text_change 17-Mar-2000 per 1995 PEMBL/DDBJ 2136.1; GSPDB:GN00028; CESP:T05A10.5</pre>		99 GKVYNKNGKTSNIANMYWDSHDKLGCAVVDCSGKTHVVCQYGPE 142 :	EERAYKSAEKCSEEPSSEEENVDVFSAATLNIPLEAGNSWMSEIFELR 98	14 DDDMREMETELHNGYRAAFARNY	90; DB 2; Length 274; D. 1.7e-18; atches 57; Indels 52; Gaps 7;	9; PIDN:AAA27789.1; PID:g440280

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protein FilC7.3 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Nov-2001
C;Accession: C89753
R;Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Tettle: Genome sequence with enematode C. elegans, and www_sanger.ac.uk/Projects/C_elegans/enematode C. elegans, and www_sanger.ac.uk/Projects/C_elegans/enematode.
A;Note: see websites genome wustl.edu/gsc/C_elegans/enematode.
A;Note: see websites genome wustl.edu/gsc/C_elegans/enematode.
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-425 (STO)
A;Cross-references: GB:chr_X; PIDN:AAC69015.1; PID:g2914120; GSPDB:GN00028; CESP:F11C7.3
C;Genee: F11C7.3
A;Map position: X
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A:Introns: 66/2: 142/3: 179/3: 208/2
C:Superfamily: cysteine-rich secreto
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hypothetical protein F49E11.9 - Caenorhabditis elegans C; Species; Caenorhabditis elegans
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Gene: CESP:T05A10.5
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Best Local :
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                                                                                                                                                                                           342 DNILTQAVFDRG--VGHYTQMAWEGTTEIGCFVENCPTFTYSVCQYGPAGNYMNQLIYTK 399
                                                                                                                                                                                                                                                                    282
                                                                                                                                                                                                                                                                                                                                         222 FTMCPSVTDQSDQARQNFLDTHNKLRTSLAKGLEADGIAAGAFAPMAKQMPKLVKYSCTV 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 AKGDGKTIYEEGAPCSRCSDYGAGVTCDDDWQNLLCI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149 QELEEFGTPIDNVLTPELWDLKGKAIGHYTQMAWDRTYRLGCGIANCPKMSYVVCHYGPA 208
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                                                                                                                                                                                                                                                                                               51 EEKAYKSAEKCSEEPSSEEE----NVDVFSAATLNIPL----EAGNSWWSEIFE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29
                                                                                                                                                                                                                                                                                                                                                                                                                  1 Similarity 23.(
45; Conservative
                                                                                                                                                                                                                                                                                                                                                                              4 YSLCQQREKLDDDMREMFTELHNGYRAAFARNYKTSKM-----RIMVYDCTL 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 LCQQREKLDDD-----KTSK 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                               ---LRGKVYNKNGKTSNIANMVWDSHDKLGCAVVDCSGKTHVVCQYGPEAKGDGKTIYEE 153
                                                                                                                                                                                                                                                                  EANARTWAKGCLYQHSTSAQRPGLGENLYMISINNMPKIQTAEDSSKAWWSELKDFGVGS 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIKMEYDCMLERFAQNWANNCVFAHSAHYERPNQGQNLYMSSFSNPDPRSLIHTAVEKWW 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LCQAPSMVKDDGGSFQCDNSLVSDVTRNFTLEQHNFYRSRLAKGFEWNGETNTSQPKASQ 88
                                                                                                                  GSPCTADADCPGTQTC
                                                                                                                                                      GAPCSRCSDYGAGVTC 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEIFE-----LRGKVYNKNGKT-SNIANMVWDSHDKLGCAVVDCSGKTHVVCQYGPE 142
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27.2%; Pred. No. 2.4
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                                                                                                                  415
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 190; DB 2;
Pred. No. 2.6e-09;
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.es 87; Indels 45;
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C;Date: 15-Oct-1999 *sequence_tevision: C;Accession: T22436
R;Baynes, C.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z19564
A;Accession: T22436
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-213 <WIL>
A;Cross-references: EMBL: 270308; PIDN:CAA94351.1; GSPDB:GN00022;
A;Experimental source: clone F49E11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Baynes, C. submitted to the EMBL Data A; Reference number: Z19564 A; Accession: T22439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein F49E11.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T22439
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A;Residues: 1-207 <WIL>
A;Residues: 1-207 <WIL>
A;Cross-references: EMBL:Z70308; PIDN:CAA94348.1; GSPDB:GN00022; CESP:F49E11.9
A;Experimental source: clone F49E11
                                                                                                                                                                                                                                                                                                                                                                       A;Introns: 14/1; 60/3; 105/3; 175/2
C;Superfamily: yellowjacket venom allergen antigen
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A; Introns: 14/1;
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Best Local Similarity
Matches 45; Conserv
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Gene: CESP:F49E11.4
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Best Local Similarity
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:Superfamily: yellowjacket venom allergen antigen
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122 LGCAVVDCSGKTH----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 AWANTSSIGCGVKNCGRDASMRNMNKIAVVCQYSPPGNTMGRPIYKEGTTCSSCS---GS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 VWDSHDKLGCAVVDCS------GKTHVVCQYGPEAKGDGKTIYEEGAPCSRCSDYGAG
                                                                                                                           72 VDVFSAATLNIPLE----AGNSWWSEIFELRG---KVYNKNGKTSNIAN---MVWDSHDK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 YGENLYWSWTSADVGSLDSYG---EIAAAAWEKEFQDFGWKSNAMDTTLFNSGIGHATQM
                                                                         91 IFWHFSSSLSTPEQYATLAPQKWWNE-FETNGWDSLIYNHASQRFQIGHAVQMAWHTTSK
                                                                                                                                                                             31 VHNEFRSQLALGQLSFRGVKKPSASMMRKISWSKKLTNAATKFAETCPKNHSVVMNTGES
                                                                                                                                                                                                           71 ------NVDVFSAATLNIPLEAGNSWWSEIFELRGKVYNK-----NGKTSNIANM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 DAHNKLRSAIAKSTYVAKGTKKEPATDMRKMVVDSTVAASAQNYANTC---PTGHSKGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 ELHNGYRAAFARNYKTSK------MRTMVYDCTLEEKAYKSAEKCSEEPSSEEE---
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                                                                                                                                                                                                                                                                            15.3%; Score 153; DB 2; Llarity 27.1%; Pred. No. 2.3e-06; Conservative 29; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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-VVCQYGPEAKGDGKTIYEEGAPCSRCSD
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                                                                                                                                                                                                                                                                                                                           Length 213;
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hypothetical protein C39E9.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T19852
R;Sims, M.
Submitted to the EMBL Data Library, March 1996
A;Reference number: Z19187
A;Reference number: Z19187
A;Recession: T19852
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-208 <WILL
A;Residues: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 8
                                                                                                                                                                                                                                                                      A; Map position:
A; Introns: 14/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein F49E11.5 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Date: 15-oct-1999 #sequence_revision 15-oct-1999 #teC; Accession: T22437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₽
                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:Z70307; PIDN:CAA94335.1; GSPDB:GN00022; A;Experimental source: clone C39E9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 4
A; Introns: 17/1; 146/3; 180/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ribaynes, C.
submitted to the EMBL Data Library, March 1996
A.Reference number: Z19564
A.Recession: T22437
                                                                                                                                                                                                                                                                                                                    Gene: CESP:C39E9.2
                                                                                                                                Matches
                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                  Superfamily: yellowjacket venom allergen antigen 5
                                                                                                                                                                                                                                                                                                                                                     Genetics
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Superfamily: yellowjacket venom allergen antigen 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150
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                                                                                                                                                                                                                                                                      14/1; 59/3; 176/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51;
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                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                 LHNGYRAAFARNYKTSK------MRTMVYDCTLEEKAYKSAEKCSEE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KSGETCSNCPD---GINCES--SIGLCV 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EEGAPCSRCSDYGAGVTCDDDWQNLLCI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLLTEELFNSGIGHATQMAWATTNKIGCGISKCSSDSFGTQYVVVCLYSPAGNYIGMDIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NGKTSNIAN------MVWDSHDKLGCAVVDCSGKTH-----VVCQYGPEAKGDGKTIY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YKSAEKCSEEPSSEEENVD-----VFSAATLNIPLEAGNSWWSEIFELRGKVYNK 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FSFCETICEFSETGKNYILSRHNYLRSQIALGKYVAGNSTKPSASNMMKLIWDTTLETTA 72
             VHNTLRSRIAKGTYVAKGTAKPAASDMLKMKWDATVAASAQAYANKCPTGHSGAAGLGEN 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QDYSTGCPTGHSASRANIGENMYWWTSPVVTQTDAELLGNRSANLWESE-FQRFG--WNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ilarity 24.
                                                                                                                         14.7%; Score 146.5; DB 2; larity 24.3%; Pred. No. 8.5e-06; Conservative 26; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.2%;
                                                                                                                      26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 152; DB 2;
Pred. No. 2.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                         Indels
                                                                                                                                                                              Length
                                                                                                                         51;
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                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129
                                                                 64
hypothetical protein C39E9.6 - Caenorhabditis elegans
(;Species; Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T19849
R;Sims, M.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z19187
A;Accession: T19849
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues; 1-210 <WILD
A;Cross-references: EMBL:Z70307; PIDN:CAA94332.1; GSPDB:GN00022; CESP:C39E9.6
A;Experimental source: clone C39E9
C;Genetics:
A;Gene: CESP:C39E9.6
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submitted to the EMBL Data Library, March 1996
A; Reference number: Z19564
A; Accession: T22438
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722438

hypothetical protein F49E11.6 - Caenorhabditis elegans
c;Species: Caenorhabditis elegans
C;Species: Coct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: 722438
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A; Introns: 58/3; 104/3; 176/2
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A;Experimental source: clone F49E11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-207 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 14.3
Best Local Similarity 23.0
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: yellowjacket venom allergen antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 YEEGAPCSRCSDYGAGVTCD 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 TLDMNTFNTGIGHATQMAWANTFAIGCGVKNCGKDPSNGYNKVAVVCQYKTPGNYLNQPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166 GVTCD 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 SQGSGYGENLYWYWTSGTIGNLDTFGPA-----ASSSWESE-----FQQYGWTSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 QQAIVDAHNKLRSSIAKGTYVAKGTTQKSGSNMRKIKWDATVATSAQNYANTC---PTGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 REMFTELHNGYRAAFARNYKTSK-----MRTMVYDCTLEEKAYKSAEKCSEEPSSE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YOOGTTCAACP---SGTACD 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----GKTHVVCQYGPEAKGDGKTI 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EE------NVDVFSAATLNIPLEAGNSWWSEIFELRGKVYNKNGKTSN 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTSCE 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.3%; suc. No. 23.0%; Pred. No. 2. 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from GB/EMBL/DDBJ
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.7e-05;
es 62; Indels
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Gaps

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RESULT 10
T19859
hypothetical protein F49E11.11 · Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T19859; T22441
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A;Introns: 58/3; 178/2
C;Superfamily: yellowjacket venom allergen antigen 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Sins, M. substitute to the EMBL Data Library, March 1996
A;Reference number: Z19187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 14.1%; Score 140.5; DB 2; Best Local Similarity 24.0%; Pred. No. 3e-05; Matches 47; Conservative 25; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Map position: 4; Introns: 15/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Introns: 15/1; 60/3; 179/2
Superfamily: yellowjacket venom allergen antigen 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecule type: DNA
Residues: 1-211 <WI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bmitted to the EMBL Data Library, March 1996
Reference number: Z19564
Accession: T22441
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: EMBL: 270308; PIDN: CAA94354.1; GSPDB: GN00022; CESP: F49E11.11 Experimental source: clone F49E11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: EMBL: 270307; PIDN: CAA94341.1; GSPDB: GN00022; CESP: F49E11.11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Experimental source: clone C39E9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecule type: DNA
Residues: 1-211 <WIL>
155 APCSRCSDYGAGVTCD 170
                                                                                                    132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                           111 IAN------MWDSHDKLGCAVVDCS------GKTHVVCQYGPEAKGDGKTIYEEG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 TGVAHATQIAWAPTGKIGCGVKNCGRDARRGGLFQVAIVCQYRVRGNFFFKNIYNSGATC 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 GKTSNIANMVWDSHDKLGCAVVDCSG-----KTHVVCQYGPEAKGDGKTIYEEGAPC 157
                                                                                                                                                                                                                                     82
                                                                                                                                                                                                                                                                                                      66
                                                                                                                                                                                                                                                                                                                                                                                                                               15 DDMREMFTELHNGYRAAFARNYKTSKMRT------MVYDCTLEEKAYKSAEKCSEEP 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E 8
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                                                                                                                                                                                                                                                                                                                                                                 22 ESTQQFIVDLHNKLRTSIAKGTYVAKGTTKAAGSNLLKMKWDTTLATAAQTFANTCPRGH 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48;
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48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DKTIGENLYWEWSGDPFSDLDKFGKIATVA-----WDHEFEQFGWNSNKFSLALFN 133
                                                                                             LANTGIGHATQMAWANTGLIGCGVKNCGPDPELNNYNRAVVVCQYKAQGNYLGQDIYKSG 191
                                                                                                                                                                                                                                 SNAAGVGENLYWRWSSLPFSGMDIYGG------AASVAWEQEFQQYG--WTTNTFTQA 131
                                                                                                                                                                                                                                                                                               SACP---AGTSCE 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KOSILNAHNDIRSRIAKGNYVAKGNRKESATNMLKMKWDSSLEQSAQNYANGCHMQHSTN 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EENV-----DVFS------AATLNIPLEAGNSWWSEIFELRGKVYNK-----N 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.2%; Score 142;
24.9%; Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23;
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red. No. 2.2e-05;
Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lenġth 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53;
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T19848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Sims, M.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z19187
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                                                                                                                                                                                                                                                                                   A;Map position: 4
A;Introns: 58/3; 177/2
C;Superfamily: yellowjacket venom allergen antigen 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypotherical protein C3989.5 - Caenorhabditis elegans
C;Speciies: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
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submitted to the EMBL Data Library, June 1996
A; Reference number: Z19943
A; Accession: T24854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: T19848
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Nolecule type: DNA; Nolecule type: DNA; Nolecule type: DNA; Nolecule type: TOP (TIL); Nolecule
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecule type: DNA
Residues: 1-262 <WIL>
                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                Gene: CESP:C39E9.5
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mes 59; Conserv
                                                                                                                                                                   Local Similarity es 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224 VVCHYWPKGNYLNEPIYLEGPPCSKCE----SKKCDK--RTGLCI 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 VVCQYGPEAKGDGKTIYEEGAPCSRCSDYGAGVTCDDDWQNLLCI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 WIKEFREKFWDSNILTNDLFGSGVGHATOMVWADTYQMGCAVSHFKEIHKRTGRPITKIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 ERSAYSFAQK---NPSQHS-----FIPDIGENLFWHWSTRPGDFNKYGPMAALS 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192 TTCSACP---TGTTCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 EIFELRGKVYNKNGKTSNI------ANMVWDSHDKLGCAVVDCS------GKTH 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 EEKAYKSAEKCSEEPSSEEENVDVFSAATLNIPLEAGNSWW------S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 DEDCEHEFMENEVAFCDNGYCNNYVPRGSQLAFG-NFVTKRHTKRAAGSNIKKFVWNATL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 DDDMREMFTE-----LHNGY------RAAFARNYKT-----SKMRTMVYDCTL 50
                               23
                                                                                             18 REMFTELHNGYRAAFARNYKTSK------MRTMYYDCTLEEKAYKSAEKCSEEPSSE
                               KQSMVNAHNAVRSSIAKGEYVAKGTKKDSATNMLKMKWDNSLAQSAQNYANGCPMQHSPD
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                                                                                                                                                                   Conservative
                                                                                                                                                                                                  13.9%;
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                                                                                                                                                               30; Mismatches
                                                                                                                                                                                              Score 138.5;
Pred. No. 4.
                                                                                                                                                                   .5e-05;
les 71;
                                                                                                                                                                                                                                     DB 2;
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                                                                                                                                                                   Indels
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223

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cysteine-rich secretory protein 2 type I precursor - human
N;Alternate names: testis-specific protein
C;Species: Homo sapiens (man)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 20-Jun-2000
C;Accession: B33329; S66682
R;Kasahara, M.; Gutknecht, J.; Brew, K.; Spurr, N.; Goodfellow, P.N.
Genomics 5, 527-534, 1989
A;Title: Cloning and mapping of a testis-specific gene with sequence similarity to a spe
A;Title: Cloning and mapping of a testis-specific gene with sequence similarity to a spe
A;Reference number: A3329; MUID:90129048; PMID:2613236
A;Accession: B3339
A;Status: preliminary
A;Molecule type: mRRA
A;Residues: 1-243 KASS
A;Cross-references: GB-M35532, NID-230882, BIDNAMAG1230 1, DID-230882
A;Cross-references: GB-M35532, NID-230882, BIDNAMAG1230 1, DID-230882
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)Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T19847
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A;Cross-references: GB.M25532; NID:9339882; PIDN:AAA61220.1; PID:9339883
R;Kraetzschmar, J.; Haendler, B.; Eberspaecher, U.; Roosterman, D.; Donner, P.; Schleun:
Eur. J. Blochem. 236, 827-856, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Introns: 14/1; 60/3; 177/2
C;Superfamily: yellowjacket venom allergen antigen 5
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A;Experimental source: clone C39E9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-209 <WIL>
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A; Accession: T19847
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Best Local S
Matches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 VGNGTQMAWAKTNLVGCGVKNCGKDSTGLNKVAVVCHYKPLGRYVDQMIYTAGFTCSQCP 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197 --- TGTSCD 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 DYGAGVTCD 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 TSNIANMVWDSHDKLGCAVVDCS-----GKTHVVCQYGPEAKGDGKTIYEEGAPCSRCS 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197 AGTSCE 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 -MYWDSHDKLGCAVVDC------SGKTHVVCQYGPEAKGDGKTIYEEGAPCSRCSDYG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83 KSYGENLFWAYSSSPITDLDKYVQSAVDTWVSE-FQMFG--WNSNKFTTALWNTGIGHAT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 ----- EEPSSEEENVDVFSAATLNIPLEAGNSWWSEIFELRGKVYNKNGK----- 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 QQFIVDLHNSFRSKLATGTYSINGTLKPAGSNIRKMSWDSTLATSAQTYANTCPTGFSNT 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 REMFTELHNGYRAAFARNYKT------SKMRTMVYDCTLEEKAYKSAEKCS----- 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 EENVDYFSAATLNIPL------EAGNSWWSEIFELRGKYYNKNGKTSNIAN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 13.8%; Score 137.5; DB 2;
Similarity 24.3%; Pred. No. 5.5e-05;
46; Conservative 21; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QGTGENLYWRTTSANISGLDIYGGA-----ASVSWEQE-FQKYGWATNYFSQELFDTG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 209;
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                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocal
                                                                                                                                                                                                                                                                                                                                      46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49;
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hypothetical protein F49E11.10 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-oct-1999 #sequence_revision 15-oct-1999 #text_change 18-Feb-2000 C;Accession: T22432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 6p21-6qter
C;Superfamily: cysteine-rich secretory protein 1
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-243/Product: cysteine-rich secretory protein 2 type I #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Title: The human cysteine-rich secretory protein (CRTSP) family. Primary structur-
A:Reference number: 568681; MUID:96270732; PMID:8665901
A:Accession: 568682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Superfamily: yellow jacket venom allergen antigen 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-243 <KRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 4
A;Introns: 58/3; 104/3; 175/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:270308; PIDN:CAA94344.1; GSPDB:GN00022; CESP:F49E11.10
A;Experimental source: clone F49E11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-207 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: Z19564
A; Accession: T22432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, March 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GDB:120760; OMIM:187430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X95239; NID:g1262816; PIDN:CAA64526.1; PID:g1262817
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CESP: F49E11.10
148 LIGCGVKDCGRDSNGLNKVTVVCQYKPQGNFINQYIYVSGATCSGCP---SGTSCE 200
                                                             121 KLGCAVVDCS-----GKTHVVCQYGPEAKGDGKTIYEEGAPCSRCSDYGAGVTCD 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 YOLL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173 WQNLL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 IAYCPNQDSLKYYYYCQYCPAGNNMNRKNTPYQQGTPCAGCPD-----DCDKGLCTNSCQ 206
                                                                                                                                      90 YWYWTSGSLGDLNQYGSAASASWEKEFQDYG--WKSNLMTIDLFNTGIGHATQMAWAKSN 147
                                                                                                                                                                                                    73 DVF----SAATLNIPLEAGNSWWSEIFELRGKVYNKNGKTSNIAN------MVWDSHD 120
                                                                                                                                                                                                                                                                         30 HNTLRSKIAKGTYVAKGTQKSPGTNLLKMKWDSAVAASAQNYANGCPTGHSGDAGLGENL 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 GENLYMSSDPTSWSSAIQSWYDEILDF---VYGVGPKSPNAVVGHYTQLVWYSTYQVGCG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38 REIVNK-HNELRKAVSP--PASNMLKMEWSREVTINAQRWANKCTLQHSDPEDRKTSTRC 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 REMFTELHNGYRAAFARNYKTSKMRTMVYDCTLEEKAYKSAEKCSEEPSSEEE----- 70
                                                                                                                                                                                                                                                                                                                                               25 HNGYRAAFARNYKTSK-----MRTMVYDCTLEEKAYKSAEKCSEEPSSEE---ENV 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 NVDVFSAATLNIPLEAGNSWWSEIFELRGKVYNKNGKTSN-----IANMVWDSHDKLGCA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                Conservative 23; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                            13.4%; Score 133.5; DB 2;
26.1%; Pred. No. 0.00012;
72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.7%; Score 137; DB 2; Length 243; 26.5%; Pred. No. 7.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28;
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                                                                                                                                                                                                                                                                                                                                                                                                                Indels 35; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 207;
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RESULT 17

A33129

testis specific protein - mouse
c:Species: Mus musculus (house mouse)
c:Species: Mus musculus (house mouse)
c:Accession: A33329
c:Accession: A33329
R:KAsshara, M.; Gutknecht, J.; Brew, K.; Spurr, N.; Goodfellow, P.N.
Genomicus 5, 527-534, 1989
A;Ritle: Cloning and mapping of a testis-specific gene with sequence similarity
A;Reference number: A33329
A;Rocession: A33329
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Molecule type: mRNA
A;Mole
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                                                                                                    A;Cross-references: GB:M2553:
C;Superfamily: cysteine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B 5
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C;Superfamily: cysteine-rich secretory protein 1
C;Superfamily: cysteine-rich secretory protein 1
F;1-19/Domain: signal sequence #status predicted <SIG>.
F;20-245/Product: neutrophil granules matrix glycoprotein SGP28 #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Kraetzschmar, J.; Haendler, B.; Eberspaecher, U.; Roosterman, D.; Donner, P.; Schleun: Eur. J. Blochem. 236, 827-836, 1996
A;Title: The human cysteine-rich secretory protein (CRISP) family. Primary structure and A;Reference number: 568681; MUID:96270732; PMID:8665901
A;Accession: 568683
                                                                                                                                    A; Molecule type: mRNA
A; Molecule type: mRNA
A; Cross:references: GB:M25533; NID:g202126; PIDN:AAA40472.1; PID:g202127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-105,'S',107-245 <KRA>
A;Cross-references: EMBL:X95240; NID:g1262818; PIDN:CAA64527.1; PID:g1262819
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A;Accession: S74313
A;Accession: type: protein
A;Besidues: 33-83;96-143;165-217;221-226 <KUL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-245 < KJE>
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Best Local S
Matches 48
                                              Query Match
Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WANQCNYRHSNPKDRMTSLKCGE-NLYMSSAPSSWSQAIQSWFDEYNDFDFGVGPKTPNA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDYGAGVTCDD 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VVGHYTQVVWYSSYLVGCGNAYCPNQKVLKYYYVCQYCPAGNWANRLYVPYEQGAPCASC 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KTSNIANMVWDSHDKLGCAVVDCSG----KTHVVCQYGPEAKGDGKTI--YEEGAPCSRC 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAEKCSEEPSSEEENVDVFSAATLNIPLEAGNSWWSEIFELRGKVYN------KNG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEDKDPAFTALLTTQTQVQREIVNKHNELRRAVSPPARN-----MLKMEWNKEAAANAQK 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.2%; Score 132;
25.1%; Pred. No. 0.
ative 22; Mismatche
              12.7%;
                                                                                                           secretory
              Score 127;
Pred. No.
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                                                                                                        protein
              7; DB 2;
. 0.00058;
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                                           Length 243
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T27833
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JC5308
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                                                                                                                                                                                                                                                                                           R; Rich,
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testis-specific, vespid, and pathogenesis-related protein 1 precursor - human C; Species: Homo sapiens (man) C; Date: 01-May-1997 #sequence_revision 01-May-1997 #text_change 19-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein zK384.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T27833
                     A; Molecule type: mRNA
A; Residues: 1-266 < RICL>
A; Cross-references: EMBL: X91911; NID:g1030052; PIDN: CAA63005.1; PID:g1030053
A; Accession: PC4311
                                                                                                                                                                                                                     Gene 180, 125-130, A; Title: RTVP-1, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; NoLecule type: DNA
A; Molecule type: DNA
A; Residues: 1-196 <WIL>
A; Cross references: EMBL: 282092; PIDN: CABO5010.1; GSPDB: GN00023; CESP: ZK384.1
A; Cross references: clone ZK384
A; Molecule type: protein
                                                                                                                                                        A;711Le: RTVP-1, a novel human gene with sequence similarity A;Reference number: JC5308; MUID:97128816; PMID:8973356 A;Ancession: JC5308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, November 1996
A; Reference number: 220427
A; Accession: T27833
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                            ;Accession: JC5308; PC4311
;Rich, T.; Chen, P.; Furman, F.; Huynh, N.; Israel, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Map position: 5
:Introns: 58/3; 95/3; 157/2
;Superfamily: yellowjacket venom allergen antigen 5
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;Gene: CESP:ZK384.1
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Best Local Similarity 24.8%; Pred. No. 0.00082;
Matches 41; Conservative 25; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 AGTKYVGCGVKRCDPINVVVVCMYYQQGNLVGRPIYKEGPPCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 DSHDKLGCAVVDCSG-KTHVVCQYGPEAKGDGKTIYEEGAPCSRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195 NCENGLCTNSCDFEDLL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 YGAGVTCDD--DWQNLL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 GHTTQLVWYSSFKIGCGIAYCPNQDNLKYFYVCHYCPMGNNVMKKSTPYQQGTPCASCPN 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 ----NMVWDSHDKLGCAVVDCSGKTHV----VCQYGPEAKGDGK--TIYEEGAPCSRCSD 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 ---EEPSSEEENVDVFSAATLNIPLEAGNSWWSEIFELRG---KYYNKNGKTSNIANMYW 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 DGLEIPIGRNIGMNYYTTKV----IDALND-WAEEFQVNGWLSTIYN-DTSISAASQMVW 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 QLSPNGRQQVLDFHNKLRSQVALGVFSANGTIKPPARNMERLTYGQQFERLAQDYVADCP 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 KLDDDMREMFTELHNGYRAAFARNYKTS-----KMRTMVYDCTLEEKAYKSAEKCS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79 CILEHSSKDDR-KINIRCGENLYMSTDPTLWSTVIQ---SWYNENEDFVYGVGAKPNSAV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 CSEEPSSEEENVDVFSAATLNIPLEAGNSWWSEIFELRGKVYNKN-----GKTSNIA- 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 EKLDDDMREMFT-----ELHNGYRAAFARNYKTSKMRTMYYDCTLEEKAYKSAEK 60
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Introns: 14/1; 59/3; 176/2
C; Superfamily: yellowjacket venom allergen antigen 5
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A:Introns: 14/1; 59/3; 176/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:Z73896; PIDN:CAA98060.1; GSPDB:GN00022; CESP:F09E8.5
A;Experimental source: clone F09E8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, May 1996
A;Reference number: Z19307
A;Accession: T20661
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F;1-21/Domain: signal sequence #status predicted <SIG>.
F;2-266/Product: testis-specific, vespid, and pathogenssis-related protein 1 #status pr
F;233-255/Domain: transmembrane #status predicted <TMM>
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C; Superfamily:
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A;Experimental source: brain tumor cell
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-208 (MIL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                      114 -----MVWDSHDKLGCAVVDCS-----GKTHVVCQYGPEAKGDGKTIYEEGAPCSRCSD 162
                                                    196 -- AGTSCE 201
                                                                                                   163 YGAGVTCD 170
                                                                                                                                         137 GHATQMAWAKTNLIGCGVKNCGMDTNGMNKVAVVCHYQPQGNYLNQNIYTSGTTCSKCP- 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 QVVWADSYKVGCAVQFCPKVSGFDALSNGAHFICNYGP--GGNYPTWPYKRGATCSACPN 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 NMVWDSHDKLGCAVVDC-----SGKTHVVCQYGPEAKGDGKT-IYEEGAPCSRCSD 162
                                                                                                                                                                                                                                    87 GENLYWYWTSGTITNIDQFGA------MASAAWEKEFQDYG--WSSNTLTMSLFNSGV 136
                                                                                                                                                                                                                                                                                 71 -----NVDVFSAATLNIPLEAGNSWWSEIFELRGKVYNKNGKTSNIAN--- 113
                                                                                                                                                                                                                                                                                                                                30 VHNTLRSRIAKGTYVARGTVKHAASDMLKMKWLRSLATSSQIYANRC---PTGHSNMIGV 86
                                                                                                                                                                                                                                                                                                                                                                            24 LHNGYRAAFAR-----NYKTSKMRTMVYDCTLEEKAYKSAEKCSEEPSSEEE---- 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 KLHPNFTSLGENIWTGSVPIFSVSS-----AITNWYDEIQDYDFKTRICKK--VCGHYT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 NEDFIKDCVRIHNKFRSEVKPT--ASDMLYMTWDPALAQIAKAWASNCQFSHNTRLKPPH 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 DDDMREMFTELHNGYRAAFARNYKTSKMRTMVYDCTLEEKAYKSAEKCS------EEP- 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 -----SSEEEN------VDVFSAATLNIPLEAGNSWWSEI--FELRGKVYNKNGKTSNIA 112
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                                                                                                                                                                                   Query Match
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A;Cross-references: GDB:683195
C;Superfamily: yellowjacket venom allergen antigen 5
C;Keywords: brain
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A;Residues: 1-219 - GMGP>
A;Cross-references: GB:U16307; NID:g1100927; PIDN:AAA82731.1; PID:g847722
A;Experimental source: brain tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Murphy, E.V.; Zhang, Y.; Zhu, W.; Biggs, J. Gene 159, 131-135, 1995
A;Title: The human joint pathogenesis-related protein is structurally related to pl A;Reference number: JC4131; MUID:95331646; PMID:7607567
A;Accession: JC4131
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submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid F02E11.
A;Reference number: Z21104
A;Accession: T31959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 02-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glioma pathogenesis-related protein - human
C; Species: Homo sapiens (man)
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A; Residues: 1-207 <FAV>
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Experimental source: strain Bristol N2; clone F02E11
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                                                                                                                                                                                                                                                  Local Similarity 25.1 ues 49; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 G----KT--SNIANMVWDSHDKLGCAVVDCS-----GKTHVVCQYGPEAKGDGKTIYEE 153
66 -----SEEEEN-----VDVFSAATLNIPLEAGNSWWSEIFELRGKVYNKNGKTSNIANM 114 :| :| :| :| :| : :
                                                                                                          20 NEDFIKDCVRIHNKFRSEVKPT--ASDMLYMTWDPALAQIAKAWASNCQFSHNTRLKPPH 77
                                                                                                                                                                                  14 DDDMREMFTELHNGYRAAFARNYKTSKMRTMVYDCTLEEKAYKSAEKCS-----EEP- 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 SAQAYANTCPTGHGKSKYGENLYWRWSGAVIKSIDDYGVRASGAWASE-FQKYGWKTNKL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 KAYKSAEKCSEEPSSEEENVDVF---SAATL----NIPLEAGNSWWSEIFELRGKVYNKN 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 GQFSKAGQKAIVD------AHNTLRSSIAKGTYVANKTRKEPGSNILKMKWDPTIAK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59/3; 175/2
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                                                                                                                                                                                                                                                      12.1%; Score 121; DB 2; Length 219; 25.1%; Pred. No. 0.0017; ative 26; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.1%; Score 121; DB 2; Length 207; 25.7%; Pred. No. 0.0016; tive 22; Mismatches 79; Indels
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                                                                                                                                                                                                                                                          Indels 46;
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A; Alternate names: CRISP-1 C; Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Species: Musculus (house mouse) C; Accession: A49202 R; Haendler, B.; Kratzschmar, J.; Theuring, F.; Schleuning, W.D. Endocrinology 133, 192-198, 1993 A; Haendler, B.; Kratzschmar, J.; Theuring, F.; Schleuning, W.D. Endocrinology 133, 192-198, 1993 A; Haendler, B.; Kratzschmar, J.; Theuring, F.; Schleuning, W.D. Endocrinology 133, 192-198, 1993 A; Flatus: Transcripts for cystelne-rich secretory protein-1 (CRISP-1; DE/AEG) and the nov A; Reference number: A49202; MUID:93307144; PMID:8319566 A; Status: preliminary A; Molecule type: nucleic acid A; Residues: 1-244 (HAED- C; Superfamily: cystelne-rich secretory protein 1 Query Match Best Local Similarity 25.4%; Pred. No. 0. 0027; Matches 51; Conservative 31; Mismatches 84; Indels 35; Gaps 10; Matches 51; Conservative 31; Mismatches 84; Indels 35; Gaps 10; Qy 3 DYSLCOOREKIDDDMREMFTELHNGYRAAFARNYKTSKMRTMYYCCTLEEKAYKSAE 59	Oy 144 KGDKTYEEGAPCSRCSDYGAGVYCDDDWONLL 177	39 SKMRTM 1 : 57 SNILKM 92 SE 117 EENENF	C.Species: Rattus norvegicus (Norway rat) C.Species: Rattus norvegicus (Norway rat) C.Species: Rattus norvegicus (Norway rat) C.Pate: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 21-Jul-2000 C.Accession: JE0204 R.Maeda, T.; Sakashita, M.; Ohba, Y.; Nakanishi, Y. Biochem. Biophys. Res. Commun. 248; 140-146, 1998 A;Title: Molacular cloning of the rat tpx-1 responsible for the interaction between sper A;Reference number: JE0204; MUID:98340864; PMID:9875100 A;Accession: JE0204 A;Molecule type: mRNA A;Residues; 1-243 CMAED A;Cross-references: DDBJ:AB009662; NID:93374579; PIDN:BAA32029.1; PID:93374580 C.Comment: This protein functions as a cell adhesion protein for the association between C;Genetics: A;Map position: 17 C;Superfamily: cysteine-rich secretory protein 1 Ouery Match Best Local Similarity 25.28; Pred. No. 0.002; Matches 41; Conservative 24; Mismatches 66; Indels 32; Gaps 8;	RESULT 23 JEO204	Qy 165 AGVTCDDDDWQNLLCI 179 188NDKCLDNLCV 197	QY 115 VWDSHDKLGCAVVDCSGKTHVVCQYGPEAKGDGKT-IYEEGAPCSRCSDYG 164	Db 78 KLHPNFTSLGENIWTGSVPIFSVSSAITNWYDEIQDYNFKTRICKKVCGHYTQV 131
D86143 D86143 hypothetical protein F6F3.11 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001 C;Accession: D86143 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alo; Chilu, C.W.; Chung, M.K.; Connu, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, Ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzi, R.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzi, R.; Li, J.H.; Li, K.; Khaykin, P.; Southwick, A.M.; Sun, H.; Tall, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Residnes: 1-28 <8700 A;Residnes: 1-28 <8700 A;Cross-references: GB:AE005172; NID:99665145; PIDN:AAF97329.1; GSPDB:GN00141	OY 51 EEKAYKSAEKCSEEPSSEEENVDVFSAATLNIPLEAGNSWGSEIFELRGKVYNKNG 106	Query Match 11.8%; Score 118; DB 2; Length 161; Best Local Similarity 26.1%; Pred. No. 0.0022; Matches 41; Conservative 21; Mismatches 41; Indels 54; Gaps 8; Matches 41; Labdamererethunger	RESULT 25 T52399 pathogenesis-related protein homolog [imported] - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-mar cress) C; Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 03-Nov-2000 C; Accession: T52399 R; Kaneko, T.; Kato, T.; Sato, S.; Nakamura, Y.; Asamizu, E.; Tabata, S. submitted to the EMBL Data Library, September 1999 A; Accession: T52399 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Status: preliminary; translated from GB/EMBL/DDBJ A; Residues: 1-161 < KANN A; Residues: 1-161 < KANN A; Cross-references: EMBL:AP000417; PIDN:BAB02556.1 A; Experimental source: cultivar Columbia C; Genetics: A; Map position: 3 C; Superfamily: pathogenesis-related leaf protein	164 197	109 SNI : 137 GHY	Qy 60 KCSEEPSSEEENVDVFSAATLNIPLEAGNSWWSEIFELRGKVYNKNGKT 108	Db 21 DSSQENRLEKLSTTKMSVQEEIVSKHNQLRRMVSPSGSDLLKMEWNYDAQVNAQQWAD 78

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A; Map position: 4
A; Note: T16L1.210
C; Superfamily: patl
F; 1-26/Domain: sign
F; 27-163/Product: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pathogenesis-related protein 1 precursor, 19.3K - Arabidopsis N;Alternate names: protein T16L1:210
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_chang
C;Accession: T04989; S71271
R.Bevan, M.; Obermater, B.; Deutschenbaur, S.; Piravandi, E.;
submitted to the Protein Sequence Database, November 1998
A;Reference number: Z15393
A;Accession: T04989
A;Molecule type: DNA
A;Residues: 1-163 <ABV>
A;Cross*references: EMBL:AL031394
A;Cross*references: EMBL:AL031394
A;Cross*references: EMBL:AL031394
A;Cross*references: EMBL:AL031394
A;Cross*references: EMBL:AL031394
A;Cross*references: EMBL:AL031394
RESULT 28
Al1085
Al1086
Al1086
C;Species: Vespula maculata (bald-faced hornet)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 11-Jan-2000
C;Accession: A31085
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A;Residues: 1-77, 'p',79-82,'L',84-88,'RL',91-92,'RR',95-162,'LLKENSI' <KLO>
A;Cross-references: EMBL:X96600; NID:g1228948; PID:g1228950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Experimental source: cultivar Columbia; BAC
R;Kloska, S.; Schuster, W.
submitted to the EMBL Data Library, March 1996
A;Reference number: 871271
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                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local :
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Map position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220 YTQIVWRDSTKVGCASVDCSNGGVYAICVYNPPGNYEGE 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 IANMVWDSHDKLGCAVVDCS-GKTHVVCQYGPEAKGDGK 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 QQREKLDDDMREMFTELHN-------GYRAAFARNYKTSKMRTMYYDCTLEEK 53
                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 24.1
38; Conservative
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                                                                                                                                                                                      VWDSHDKLGCAVVDC-SGKTHVVCQYGPEAKGDGKTIY 151
                                                                                                                                                                                                                                                                                                                                                                            DMREMFTELHNGYR--------AAFARNYKTSKMRTMVYDCTLEEKAYKSAEKC
                                                                                                                                                                  VWRNSERLGCAKVRCNNGQTFITCNYDPPGNWVGEWPY 163
                                                                                                                                                                                                                                                 ----GSYGENIAWSSGSMTGV--AAVDMWVDEQFD----YDYDSNTCAWDKQCGHYTQV
                                                                                                                                                                                                                                                                                        SEEPSSEEENVDVFSAATLNIPLEAGNSWWSEIFELRGKVYNKNGKT-----SNIANM
                                                                                                                                                                                                                                                                                                                                       DSPQDFLAVHNRARAEVGVGPLRWDEKVAAYARNYANQRKG----DCAMKHSS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                            11.3%;
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Pred. No. 0
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                      53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E.; Hoheisel, J.; Mewes,
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RESULT 30
B44583
C; Accession: B44583; A44522
R; Hoffman, D.R.
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T21763
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Proc. Natl. Acad. Sci. U.S.A. 85, 895-899, 1988
A;Title: CDNA cloning and primary structure of a white-face hornet venom
A;Reference number: A94213; MUID:88124947; PMID:3422469
A;Accession: A3108
A;Accession: T227 <FRNA
A;Residues: 1-227 <FRNA
A;Residues: 1-227 <FRNA
A;Cross-references: GB:JU0540cket venom allergen antigen 5
E;1-23/Domain: Signal sequence #status predicted <MAT>
E;24-227/Product: antigen 5-2 #status predicted <MAT>
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R;Steward, C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, A; Reference number: 219470
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                                                                                                                                                                                                                                                                          195 MHRSWSSKEITDLDIYGT-----KAAESWAGE-FQKKGWESNIYTKDTEKSGIGHATQ
                                                                                                                                                                                                                                                                                                                                                          135 KIHNDLRSEIAKGLFLAKGIEKPPASDMMKISWDDSIAESAQTFIEKCPMNHTKTEYGEN 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 NIANMYWDSHDKLGCA---VVDCSGKTH-VVCQYGPEAKGDGKTIYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 FNHDDCRNTAKYQVGQNIAISSTTATQFDRPSKLIKQWEDEVTEFNYKVGLQNSNFRKVG
                                                                                                                                                                                                                                                                                                                                                                                                23 ELHNGYRAAFARNY-----KTSKMRTMVYDCTLEEKAYKSAEKCSEE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 LTNDEKNEILKRHNDFRONVAKGLETRGKPGPOPPAKNMNVLVWNDELAKIAOTWANOCD 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                             MVWSQAYLIGCGVKDCGPDKTKKNMHKITVVCRY
                                                                                                                                                                                                                                    MVWDSHDKLGCAVVDCS-----GKTHVVCQY 139
                                                                                                                                                                                                                                                                                                                   ----PSSEEENVDVFSAATLNIPLEAGNSWWSEIFELRG---KVYNKNGKTSNIAN---
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                                                                                                                                                                                                                                                                                                                                                                                                                                       11.3%; Score 112.5; D
24.7%; Pred. No. 0.02;
tive 21; Mismatches
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                                                #text_change 11-Jan-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                          246
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RESULT 32

REAUTH 32

REAUTH 32

Venom allergen antigen Ves vi 5 - yellowjacket (Vespula vidua)

C;Species: Vespula vidua

C;Decies: Vespula vidua

C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 11-Jan-2000

C;Accession: E44583; E44522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-202 <HOF>
C;Superfamily: yellowjacket venom allergen antigen 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Allergy Clin. Immunol. 92, 707-716, 1993
A;Title: Allergens in hymenoptera venom XXV: the amino acid sequences A;Reference number: A44583; MUID:94044316; PMID:8227862
A;Accession: B44583
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-204 <400F>
C;Superfamily: yellowjacket venom allergen antigen 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Hoffman, D.R. Immunol. 92, 707-716, 1993
7. Allergy Clin. Immunol. 92, 707-716, 1993
A;Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 molec A;Ritle: number: A44583; MUID:94044316; PMID:8227862
A;Accession: H44583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 31
H44583
venom allergen antigen Vesp c 5.02 - European hornet
c;species: Vespa crabro (European hornet)
c;species: Voun-1994 #sequence_revision 27-Jun-1994 #text_change 11-Jan-2000
c;hoccession: H44583; H44522
                                                       R;Hoffman, D.R. Immunol. 92, 707-716, 1993
J. Allergy Clin. Immunol. 92, 707-716, 1993
A;Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 moled A;Reference number: A44583; MUID:94044316; PMID:8227862
A;Accession: E44583
                                       A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 37
                    Molecule
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                                                                                                                                                                                                                                                                                                                                                   115
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                                                                                                                                                                                                                                                                                                               159
                                                                                                                                                                                                                                                                                                                                                                                          108
type: protein : 1-206 <HOF>
                                                                                                                                                                                                                                                                                                                                                                                                                               62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 HNGYRAAFARNYKT------SKMRTMYYDCTLEEKAYKSAEKC--------61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 YSLCQQREKLDDDMREMFTELHNGYRAAFARNYKT-----SKMRTMVYDCTLEEK 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 -----SEEPSSEEENVDVFSAATLNIPLEAGNSWWSEIFELR-GKVYNKNGKTSNIANM 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SENNFLKIGHYTOMVWANTKEVGCGSIKYIODKWHKHYLVCNYGPSGNFGNEELYQ 202
                                                                                                                                                                                                                                                                                                                                                   VWDSHDKLGCA----VVDCSGKTHVVCQYGPEAKGDGKTIYE 152
                                                                                                                                                                                                                                                                                                                                                                                        SVGQNIAEGSTSADNFVNVSNMVKM------WEDEVKDYQYGSPKNKLNKVGHYTQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HNEFROKVARGLETRGNPGPOPPAKSMNTLVWNDELAQIAOVWANQCNYGHDNCRNSAKY 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NKNG--KTSNIANMVWDSHDKLGCA----VVDCSGKTHVVCQYGPEAKGDGKTIYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AYKSAEKC-----SEEPSSEEENVDVFSAATLNIPLEAGNSWWSEIFELR-GKVY 102
                                                                                                                                                                                                                                                                                                               VWAKTKEIGCGSEDYIEDGWHRHYLVCNYGPAGNVGNEPIYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQVWANQCQYGHDTCRDVAKYPVGQNVALTGSTAAKYDNPVKLVKMWEDEVKDYNPKKKF 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YGLTKQEKQ--DILKE-----HNDFRQKIARGLETRGNPGPQPPAKNMKNLVWSDELAYI 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.2%; Score 111.5; DB 22.8%; Pred. No. 0.011; ative 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.2%;
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B31085
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                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-213 <FAN>
                                                                                                                A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-205 <HOF>
                    Query Match
Best Local S
Matches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 40
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Best Local (
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38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 Similarity 23.4
40; Conservative
                h 10.9%; Score 108.5; DB 2; Similarity 23.3%; Pred. No. 0.021; 38; Conservative 29; Mismatches 67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30;
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Indels

29;

Gaps

7;

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RESULT 34
D44583
P4583
venom allergen antigen Ves s 5 - southern yellowjacket
C; Species: Vespula squamosa (southern yellowjacket)
C; Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 11-Jan-2000
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 11-Jan-2000
C:Darcession: D44583; D44522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: yellowjacket venom allergen antigen 5 F;1-10/Domain: signal sequence #status predicted <SIG>F;11-213/Product: antigen 5-3 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antigen 5-3 precursor - bald-faced hornet (fragment)
C;Species: Vespula maculata (bald-faced hornet)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 11-Jan-2000
C;Accession: B31085
R;Fang, K.S.Y.; Vitale, M.; Fehlner, P.; King, T.P.
Proc. Natl. Acad. Sci. U.S.A. 85, 895-899, 1988
A;Title: cDNA cloning and primary structure of a white-face hornet venom al:
A;Reference number: A94213; MUID:88124947; PMID:3422469
                                                                                                                                                                         C;Accession: D44583; D44522
R;Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
J. Allergy Clin. Immunol. 92, 707-716, 1993
A;Title: Allergens in hymenoptera venom XXV: the amino acid A;Reference number: A44583; MUID:94044316; PMID:8227862
A;Accession: D44583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 FGHDQCRNTEKYQVGQNVAIASTTGNSYATMSKLIE---MWENEVKDFNPKKGTIGDNNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 GKTSNIANMVWDSHDKLGCA---VVDCSGKTH-VVCQYGPEAKGDGKTIYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 NIANMYWDSHDKLGCA---VVDCSGKTH-VVCQYGPEAKGDGKTIYEE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 LDDDMREMFTELHNGYRAAFARNYKT-----SKMRTMYYDCTLEEKAYKSAEKCS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 LTEAEKQEILKVHNDFRQKVAKGLETRGNPGPQPPAKNMNNLVWNDELANIAQVWASQCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 LDDDMREMFTELHNGYRAAFARNYKT-----SKMRTMVYDCTLEEKAYKSAEKCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 VSNDEKNEIVNRHNQFRQKVAKGLETRGNPGPQPPAKNMNVLVWNDELAKIAQTWANQCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98 YGHDTCKDTEKYPYGQNIAKRSTTAALEDSPGKLYKMWENEVKDENPNIEWSKNNLKKTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 -- EEPSSEEENVDV-----FSAATLNIPLEAGNSWWSEIFELRGKV-YNKNG--KTS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKYGHYTOMYWGKTKEIGCGSYKYIENNWHTHYLYCNYGPAGNYMDQPIYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------EEPSSEEENVDVFSA-----ATLNIPLEAGNSWWSEIFEL---RGKVYNKN- 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYTOMVWAKTKEIGCGSVKYVKDEWYTHYLVCNYGPSGNFRNEKLYEK
                                                          yellowjacket venom allergen antigen 5
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72;
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Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                   sequences
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      205;
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                                                                                                                                                                                                                                       of antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162
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밁 Ş 밁 8 ₽ Ş

202

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antigen 5 - eastern yellowjacket
C;Species: Vespula maculifrons (eastern yellowjacket)
C;Date: 06.Nov-1992 #sequence_revision 06-Nov-1992 #text_change 11-Jan-2000
C;Accession: B37329
R;Lu, G.; Villalba, M.; Coscia, M.R.; Hoffman, D.R.; King, T.P.
submitted to the Protein Sequence Database, August 1992
A;Reference number: A37329
A;Accession: B37329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein ZK384.2 - Caenorhabditis elegans
; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C; Paccession: T27834
R; Alascough, R.
submitted to the EMBL Data Library, November 1996
A; Reference number: Z20427
A; Rocession: T27834
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                A;Status: preliminary
A;Molecule type: protein
A;Residues: 1·204 <LUI>
C;Superfamily: yellowjacket venom allergen antigen 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-212 <WIL>
A;Cross-references: EMBL:ZB2092; PIDN:CAB05011.1; GSPDB:GN00023; CESP:ZK384.2
A;Experimental source: clone ZK384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 47
Query Match
Best Local S
Matches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetics:
Gene: CESP:ZK384.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :Introns: 60/3; 106/3; 180/2
:Superfamily: yellowjacket venom allergen antigen 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           192 GPTCSACP---ASTKCE 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 GAPCSRCSDYGAGVTCD 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 GDHRLLTSATQMVWATTRHVGCGVNICDAEKNLFGYRNKVVVVICEYQSKGNIHGLPIYKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 TC---PSLFTDSKMLGRNYYHRLANVTSGSLDKYALFAVKKWERQ-FQERGWKNQEFRMF 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 KCSEEPSSEEEN------VDVFSAATLNIPLEAGNSWWSEIFELRG-----KVY 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 QREKLDDDMREMFTELHNGYRAAFAR-NY-----KTSKMRTMYYDCTLEEKAYKSAE 59
18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MVWDSHDKLGCA---VVDCSGKTH-VVCQYGPEAKGDGKTIYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NKNGKTSNIANMVWDSHDKLGCAVVDCS-----GKTHVVCQYGPEAKGDGKTIYEE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QREIVD-----FHNSLRSQLANGDYVVDGVPKPPAKDMMKMKWDPILAGMAKNNAA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MVWAKTKEIGCGSIKYVDNNWYTHYLVCNYGPAGNFGNQEVYE 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CKDTTKYNVGQNIAV-SSSTAAVYENVGNLVKAWENEVKDFNPTISWEQNEFKKIGHYTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --SEEPSSEEENVDVFSAATLNIPLEAGN---SWWSEIFELRGKV---YNKNGKTSNIAN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KQEILKIHNDFRNKVARGLETRGNPGPQPPAKNMNNLVWNNELANIAQIWASQCKYGHDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REMFTELHNGYRAAFARNYKT------SKMRTMVYDCTLEEKAYKSAEKC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                     10.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.9%; Score 108.5;
23.9%; Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24; Mismatches
Score 107; DB
Pred. No. 0.02
14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ປ.022;
75;
                  DB 2; Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
70;
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Indels
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34,
Gaps
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7;
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T24999
                                                                                                                                                                                                                                            venom allergen antigen Ves f 5 - yellowjacket (Vespula flavopilosa)
C;Species: Vespula flavopilosa
C;Date: 27-dun-1994 #sequence_revision 27-Jun-1994 #text_change 11-Jan-2000
C;Accession: A44583; B44522
                                          A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-204 <HOF>
C;Superfamily: yellowjack
                                                                                                                                R;HOffman, D.R.

J. Allergy Clin. Immunol. 92, 707-716, 1993
A;Title: Allergens in hymenoptera venom XXV: the amino acid sequences
A;Reference number: A44583; MUID:94044316; PMID:8227862
A;Accession: A44583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein T19C9.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Decies: Coct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C;Accession: T24999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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A;Reference number: Z19967
A;Accession: T24999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                map position: 5
:Introns: 64/3; 109/3; 176/2
:Superfamily: yellowjacket ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: EMBL:292972; PIDN:CAB07484.1; GSPDB:GN00023; CESP:T19C9.
EXPERIMENTAL SOURCE: Clone T19C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecule type: DNA Residues: 1-212 <WIL>
                                        Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103 NKNG--KTSNIANMVWDSHDKLGCA----VVDCSGKTHVVCQYGPEAKGDGKTIYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166 GVTCDDD 172
                                                                                                                                                                                                                                                                                                                                                                                                                                  197 GTSCGTD 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 LYSKSKSIGCIYESCDKIDSKGINYNTRLLICKYSPPLENIDEKLEDKGEPCSNCP---S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88 ----NLPIKLGDN----IYQYDVNTYDDIDGVGAMGSINKDTHDALKSEAKAAKNRLRQM 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 AATLNIPLEAGNSWWSEIFELRGKVYNKNGKTSNIANMVWDSHDKL-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 LHNGYRAAFARNY-----KTSKMRTMVYDCTLEEKAYKSAEKCSEEPSSEEENVDVFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GCAVVDCSGKTH----VVCQYGPEAKGDGKTIYEEGAPCSRCSDYGA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IHNKLRNAASHGLWERHSISKSSNWOLLSWNESLVAEAENEKYYC--EPADNK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SENNFLKIGHYTQMVWANTKEVGCGSIKYIQENWHKHYLVCNYGPSGNFQNEELYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQVWANQCQYGHDTCRDVAKYQVGQNVALTGSTAAVYNDPVKLVKMWEDEVKDYNPKKKF 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AYKSAEKC-----SEEPSSEEENVDVFSAATLNIPLEAGNSWWSEIFELR-GKVY 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YGLTKQEKQ--DILKE-----HNDFRQKIARGLETRGNPGPQPPAKNMKNLVWSDELAYI 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YSLCQQREKLDDDMREMFTELHNGYRAAFARNYKT-----SKMRTMVYDCTLEEK 53
                                          yellowjacket venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.7%; Score
18.7%; Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 107;
Pred. No. 0
Score
                                        allergen antigen 5
106;
DB
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58;

Indels 58;

122 87 76

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2,

Length 204;

of antigen

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000 C:Accession: 723676 R:Geisel, C:; Bradshaw, H. submitted to the EMBL Data Library, July 1996 A:Description: The sequence of C. elegans cosmid C50E3. A:Reference number: Z20662 A:Accession: 723676 A:Status: preliminary; translated from GB/EMBL/DDBJ A:McCesle type: DNA A:Residues: 1-208 dCEI> A:Cross references: EMBL:U64848; PIDN:AAB04885.1; GSPDB:GN00023; CESP:C50E3.10 A:Experimental source: strain Bristol N2; clone C50E3 A:Genetics: C50E9:C50E3.10 A:Map position: 5 A:Introns: 60/3; 103/3; 170/2 A:Map position: 5 C:Superfamily: yellowjacket venom allergen antigen 5 C:Superfamily: yellowjacket venom allergen antigen 5 Ouery Match Duery Match Best Local Similarity 21.7%; Pred. No. 0.045;	Qy 63EBPSSEBENNOVFSAATLNIPLEAGNISMSEITELR-GKYVKKUKTSHIANAVMDS 118	Superfamily: yellowjacket venom allergen antigen 5 Superfamily: yellowjacket venom allergen antigen 5 Guery Match 10.6%; Score 105.5; DB 2; Length 202; Guery Match Best Local Similarity 22.2%; Pred. No. 0.039; Best Local Similarity 22.2%; Conservative 26; Mismatches 62; Indels 35; Gaps Matches 35; Conservative 26; Mismatches 62; Indels 35; Gaps Matches 35; Conservative 26; Mismatches 62; Indels 35; Gaps Matches 35; Conservative 16; Mismatches 62; Indels 35; Gaps Matches 35; Conservative 16; Mismatches 62; Indels 35; Gaps Matches 35; Conservative 16; Mismatches 62; Indels 35; Gaps Matches 35; Conservative 16; Mismatches 62; Indels 35; Gaps Matches 35; Conservative 16; Mismatches 62; Indels 35; Gaps Matches 35; Conservative 16; Mismatches 62; Indels 35; Gaps Matches 35; Conservative 16; Mismatches 62; Indels 35; Gaps Matches 35; Conservative 16; Mismatches 62; Indels 35; Gaps Matches 35; Conservative 16; Mismatches 62; Indels 35; Gaps	SULT 39 4583 4683 bate: 27-Jun-19 Bate: 27-Jun-19 Accession: 64456 Hoffman, D.R. Allergy Clin. Title: Allergen Reference number Accession: 64456 Status: prelimit Molecule type: Pagidnes: 1-202	Best Local Similarity 21.6%; Pred. No. 0.035; Matches 38; Conservative 35; Mismatches 69; Indels 34; Gaps 7; Qy 4 YSLCQOREKLDDDMREMFTELHNGYRAAFARNYKTSKMRTMYVDCTLEEK 53
143 LSRYDSRIGHATOILWKETRKIGCAVOECPARQOGSLDGOKY 147 GKTIYEEGAPCSRCSDYGAGVTCDDDWQ 174	OURTY MAICH OURTY MAICH 10.5%, SCOTE 105; DB 2; LEN9th 241; Best Local Similarity 21.6%, Pred. No. 0.053; Best Local Similarity 21.6%, Pred. No. 0.053; Matches 46; Conservative 27; Mismatches 90; Indels 50; Gaps 7; Out 10 REKLDDDMREMETELHNGYRAAFARNYKTSKMRTMVYDCTLEEKAYKSAEK 60	A; Accession: 13339/ A; Status; preliminary; translated from GB/EMBL/DDBJ A; Status; preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Residues: 1-241 <roh> A; Cross: references: EMBL: AF078781; pIDN: AAC26915.1; GSPDB: GN00022; CESP: B0545.3 A; Experimental source: strain Bristol N2; clone B0545 C; Genetics: A; Genetics: CESP: B0545.3 A; Genetics: CESP: B0545.3 A; Genetics: A; Genetics: A; Genetics: CESP: B0545.3 A; Genetics: CESP: B0545.3 A; Genetics: CESP: B0545.3 A; Genetics: CESP: B0545.3 A; Genetics: CESP: B0545.3</roh>	Qy 168 TCDDWQNL 176 Db 194 SCTDPWMKL 202 RESULT 41 T33397 hypothetical protein B0545.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C;Accession: T33397 R;Rohlfing, T. submitted to the EMBL Data Library, July 1998 A;Description: The sequence of C. elegans cosmid B0545. A;Reference number: Z21337 A;Reference number: Z21337	Matches 41; Conservative 30; Mismatches 72; Indels 46; Gaps 8; Qy 12 KLDDDMREMFTELHNGYRAAFARNYKTSKMRTMVYDCTLEEK

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venor allergen antigen Ves p 5 - western yellowjacket
C;Species: Vespula pensylvanica (western yellowjacket)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 11-Jan-2000
C;Accession: C44583; C44522
R;Hoffman, D.R.
J Allergy Clin. Immunol. 92, 707-716, 1993
J, Allergy Clin. Immunol. 92, 707-716, 1993
A;Fitle: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 april 1.
A;Fitle: Allergens in 44583; MUID:94044316; PMID:8227862
A;Accession: C44583
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-204 4CDP2
A;Residues: 1-204 4CDP2
C;Superfamily: vellouis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-312 <KIR>
A;Residues: 1-312 <KIR>
A;Cross-references: EMBL:U23514; NID:9746484; PID:9746485; PIDN:AAC46538.1;
A;Experimental source: strain Bristol N2
C;Genetics:
C;Genetics:
A;Gene: CESP:P48E8.1
A;Introns: 28/1; 94/3; 153/3; 174/3; 226/3
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Best Local S
Matches 41
RESULT 44

T20581
hypothetical protein F08E10.7 - Caenorhabditis elegans
c;Species; Caenorhabditis elegans
c;Species; Caenorhabditis elegans
c;Species; Coct-1999 #sequence_revision 15-Oct-1999 #text_change (c;Daccession: T20581
c;Accession: T20581
b;Reference number: Z19296
A;Reference number: Z19296
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local S
Matches 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EGDYSLCOOREKLDDDMREMFTELHNGYRAAFARNYKTSKMRTMVYDCTLEEKAYKSAEK 60
                                                                                                                                                                                                                  153 KIGHYTQMVWANTKEIGCGSIKYIQNEWHKHYLVCNYGPSGNFGNEELYQ 202
                                                                                                                                                                                                                                                   107 KTSNIANMVWDSHDKLGCAVVDCS----GKTHVVCQYGPEAKGDGKTIYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 10.5%; Score 105; DB 2; Length 312; Similarity 21.7%; Pred. No. 0.073; 41; Conservative 30; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                     93
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                                                                                                                                                                                                                                                                                                                                                                                                                  ch 10.3%; Score 103; DB 2; Length 204; I Similarity 20.6%; Pred. No. 0.066; 35; Conservative 31; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHDKLGCAVVDCS-----GKTH---VVCQYGPEAKGDGKTIV------151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CSEEPSSEEENV--DVFSAATLNIPLEAGNSWWSEIFELR-GKVYNKNGKTSNIANMVWD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GDNGKCSNC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EEGAPCSRC 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KINLVGCGFSRCRDVQGVWGRGHRNVFVCHYNPQ----GNTVFVTARGQLYAMPAFTWAS 234
                                                                                                                                                                                                                                                                                                                                                   KEEKODILKE-----HNDFROKIARGLETRGNPGPOPPAKNMKNLVWNDELAYVAQVWAN 92
                                                                                                                                                                                                                                                                                                                                                                                   REKLDDDMREMETELHNGYRAAFARNYKT-----SKMRTMYYDCTLEEKAYKSAE
                                                                                                                                                                                                                                                                                   QCQYGHDTCRDVAXYPVGQNVALTGSTADKYDNPKLVKMWEDEVKDYNPKKKESENNEN 152
                                                                                                                                                                                                                                                                                                                    KC-----SEEPSSEEENVDVFSAATLNIPLEAGNSWWSEIFELRGK---VYNKNG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80; Indels 38;
                                                                                                                                                                                                                                                                                                                                                                                                                              72; Indels 32;
                                                                                                                  04-Mar-2000
                                                                                                                                                                                                                                                                 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                    59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Map position: 5
A;Introns: 64/3; 109/3; 176/2
C;Superfamily: yellowjacket venom allergen antigen 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: CESP:F08E10.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 45
B37330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
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Best Local S
Matches 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88
                                                                                           112
                                                                                                                          100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 19.36; Conservative
                                                                                                                                                           65
                                                                                                                                                                                           40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GISCGID 203
                                                           KVEHYTQIVWAKTSKIGCARIMFKEPDNWTKHYLVCNYGPAGNVLGAPIYE 209
                                                                                         ----ANMVWDSHDKLGCAVV-----DCSGKTHVVCQYGPEAKGDGKTIYE 152
                                                                                                                          HDA-CRNVERFAVGQNIAATSSSGKNKSTPNEMILLMYNEVKDFDNRWISSFPSDDNILM 158
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A;Molecule type: DNA
A;Residues: 1-212 <WIL>
A;Residues: 1-212 <WIL>
A;Cross-references: EMBL:AL021566; PIDN:CAA16500.1; GSPDB:GN00023; CESP:F08E10.7
A;Experimental source: clone F08E10
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 LYSKSKSIGCIYESCDKIDSKGINYNTRLVICKYSPPLENIDEQLFDKGEPCSNCP---S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37 IHNKLKNAASHGLWERYSISKSSNWQLLSWNESLVAEVENEKYYC--EPADNK------ 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 LHNGYRAAFARNY-----KTSKMRTMYYDCTLEEKAYKSAEKCSEEPSSEEENVDVFS 76
                                                    15 DDMRENFTELHNGYRAAFARNYK-----TSKNRTMYYDCTLEEKAYKSAEKCSEE 64
                                                                                ch 10.1%; Score 101; DB 2; Length 212; 1 Similarity 24.6%; Pred. NO. 0.1; 42; Conservative 23; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VWDSHDKLGCAV-----VDCSGKTH-----VVCQYGPEAKGDGKTIYEEGAPCSRCSDYGA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----NLPIKLGDN----IYQYDVNTYDDIDGVGAMGSINKDTHNALKSEEKATKNRLROM 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATLNIPLEAGNSWWSEIPELRGKYYNK------NGKTSN------IANM 114
PSSEEENVDVFS----AAT-----LNIPLEAGNSWWSEIFELRGKVYNKNGKTSNI-- 111
                          DAEKDATVNKHNELRORVASGKEMRGTNGPOPPAVKMPNLTWDPELATTAORWANOCTFE 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.3%; Score 103; DB 2; Length 212; 19.3%; Pred. No. 0.069; tive 35; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 58;
                                                                                             Indels 34;
                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                               of imported i
                                                                                                                                                                                                                                              species
                                                                                                  6
                                                                                                                                                                                                                                                of.
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Search completed: July 15, 2003, 08:34:55 Job time: 42 secs

Title: Perfect score: Sequence:

US-09-937-555A-2

EGDYSLCQQREKLDDDMREM.....DYGAGYTCDDDWQNLLCIGH

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Š

protein

protein search, using sw model

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen

July 15, 2003, 08:32:07; Search time 23 Seconds (without alignments) 326.401 Million cell updates/sec

on:

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RESULT 1

ASP_ANCCA

AC 0.6537;
DT 01-ROV-1997 (Rel. 35, Last sequence update)
DT 01-ROV-1997 (Rel. 35, Last sequence update)
DT 01-ROV-1997 (Rel. 35, Last sequence update)
DT 30-RAY-2000 (Rel. 39, Last annotation update)
DE Ancylostoma secreted protein precursor.
GN ASP, ON Rel. 39, Last annotation update)
DE Ancylostoma caninum (Dog hookworm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rha
OC Ancylostomatoidea; Ancylostomatidae; Ancylostom
OX RIJ_TAXID-29170;
RN [1]
RN MEDLINE-96215086; Pubmed-8636085;
RX MEDLINE-96215086; Pubmed-8636086;
RX MEDLINE-96215
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RA HAWDON J.M., Jones B.F., Hoffman D.R., Hotez P.J.;

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RA HAWDON J.M., Jones B.F., Hoffman D.R., Hotez P.J.;

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RA HAWDON J.M., Jones B.F., Hoffman D.R., Hotez P.J.;

RA HAWDON J.M., Jones B.F., Hoffman D.R., Hotez P.J.;

RA HAWDON J.M., Jones B.F., Hoffman D.R., Hotez P.J.;

RA HAWDON J.M., Jones B.F., Hoffman D.R., Hotez P.J.;

RA HAWDON J.M., Jones B.F., Hoffman D.R., Hotez P.J.;

RA HAWDON J.M., Jones B.F., Hoffman D.R., Hotez P.J.;

RA HAWDON J.M., Jones B.F., Hoffman D.R., Hotez P.J.;

RA HAWDON J.M., ASSOCIATED WITH THE TRANSITION TO PARASITISM BY J. HOLE TO
                                                                                                                           Query Match
Query Match
Similarity 32.5%; Pred. No. 2e-16;
Matches 62; Conservative 27; Mismatches 71;
                                                                                                                                                                                                                                                   EMBL; U26187; AAC47001.1; ...

RISSP; P04284; 1CFE.

InterPro; IPR01283; Allrgn_V5/Tpx1.

Pfam; PF00188; SCP; 1.

PFINTS; PR00837; V5TPXLIKE.

PFODOM; PD000542; Allrgn_V5/Tpx1; 2.

SMART; SM0198; SCP; 2.

SMART; SM0198; SCP; 2.

PROSITE; PS01009; SCP_AG5_PR1_SC7_1; FALSE_NEG.

PROSITE; PS010109; SCP_AG5_PR1_SC7_2; FALSE_NEG.

PROSITE; PS010109; SCP_AG5_PR1_SC7_2; FALSE_NEG.

ROSITE; PS01010; SCP_AG5_PR1_SC7_2; FALSE_NEG.

PROSITE; PS01010; SCP_AG5_PR1_SC7_2; FALSE_NEG.

ROSITE; PS01010; SCP_AG5_PR1_SC7_2; FALSE_NEG.

SIGNAL 1 1 B POTENTIAL.

SIGNAL 1 1 424 AN; 45735 MW; 48C8295F5D3035F9 CR
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ASP.
ASP.
Ancylostoma caninum (Dog hookworm).
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Ancylostomatoidea; Ancylostomatidae; Ancylostomatinae; Ancylostoma.
NCBI_TaxID=29170;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CPSNTGMTDSVRDTFLSVHNEFRSSVARGLEPDALGGNAPKAAKMLKMVYDCEVEASAIR
                                                         CQQREKLDDDMREMFTELHNGYRAAFARNY-----KTSKMRTMVYDCTLEEKAYK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIZ_HORVU
PRIJ_HORVU
PRIJ_HORVU
PRIJ_HORVU
PRIL_TOBAC
PRIL_HORVU
VAS_POLEN
VAS_POLEN
VAS_POLAN
ITBS_HUMAN
PRI_ARATH
PRIL_TOBAC
PRIB_TOBAC
                                                                                                                                                                                                                                                   POTENTIAL.
ANCYLOSTOMA SECRETED PROTEIN.
3 4BC8295F5D3035F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
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                                                                                                                                                                                     Length 424;
                                                                                                                               Indels 31;
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P35793
P35793
P81657
P08299
Q05968
Q051759
Q051080
P180104
P13154
P09042
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hordeum vul
hordeum vul
hordeum vul
cotiana t
hordeum vul
286
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Result No.

Score

Length

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Description

7 ancylostoma
0 equus cabal
5 heloderma h
2 homo sapien
8 homo sapien
3 mus musculu
6 polistes do
0 homo sapien
1 mus musculu
6 dolichovesp

145.5 137.5 137.5 137.5 137.5 137.1

126.6 133.8

ASP_ANCGA
CRS3_HORSE
HELO_HELHO
TPX1_HOMAN
CRS3_HUMAN
CRS3_HUMAN
TPX1_MOUSE
VA5_POLDO
GLIF_HUMAN
AEG1_MOUSE
VA52_VESGE
VA52_VESGE
VA52_VESGE
VA53_VESGE
VA53_VESGE
VA54_VESGE
VA55_VESGE
VESGE
VA55_VESGE
VESGE
VESGE
VA55_VESGE
VESGE
VE

P81656

4 vespula ger
2 vespa crabr
7 cavia porce
7 vespula vid
6 vespula squ
7 dolichovesp
5 trimeresury
5 trimeresury
6 vespula mac
1 vespula mac
1 vespula pen
1 vespula vil
1 vespula vil
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2 vespula vil
3 vespula vil
6 caenorhabdi
5 vespula vil
6 caenorhabdi
5 vespula vil
7 mus musculu
8 dolichovesp
0 listes fu
2 saccharomyc
9 sambucus ni
7 homo sapien
7 homo sapien

Database

SwissProt_40:*

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Total number of

hits satisfying chosen parameters:

112892

112892 seqs, 41476328 residues

DB seq

length: 0 length: 2000000000

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west Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                    SHART; SM00198; SCP, 1.
PROSITE; PS01000; SCP_AG5_PR1_SC7_1; 1.
PROSITE; PS010101; SCP_AG5_PR1_SC7_2; 1.
Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AJ001400; CAA04779.1; -.
HSSP; P04284; 1CFE.
InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam; PF00188; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Equis caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   )19010;
15-7UI-1998 (Rel. 36, Created)
15-7UI-1998 (Rel. 36, Last sequence update)
16-9CT-2001 (Rel. 40, Last annotation update
                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochim.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98422318; PubMed-9748582;
Schambony A., Gentzel M., Wolfes
Toepfer-Petersen E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRS3_HORSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIFIC GRANULES (BY SIMILARLY).

TISSUE SPECIFICITY: EXPRESSED IN THE SALIVARY GLAND, IN THE AMPULLA AND THE SEMINAL VESICLE.

AMPULLA AND THE SEMINAL VESICLE.

SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TEX1;
INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.

INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       him. Blophys. Acta 1387;206-216(1998).
SUBCELIUIAR LOCATION: SECRETED; IN NEUTROPHILS, LOCALIZED IN
SPECIFIC GRANULES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00188; SCP; 1.
m; pD000542; Allrgn_V5/Tpx1; 1.
; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    407
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73
                                                             36
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                                                                                                                                                                        48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRISP-3: primary structure and expression in the male genital
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KVYNKNG-KTSNIANMVWDSHDKLGCAVVDCSGKTHVVCQYGPEAKGDGKTIYEEGAPCS 158
         -----DVFSAATLNIPLEAGNSWWSEIFELRGKVYNKNGKTSN-----IANWVWDSHDKL
                                                          EVQKEIVNKHNDLRRTVSP--LASNMLKMQWDSKTATNAQNWANKCLLQHSKAEDRAVGT
                                                                                                                    DMREMFTELHNGYRAAFARNYKTSKMRTMVYDCTLEEKAYKSAEKCSEEPSSEEENV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QCS---PGATC 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HGNKCVYQHSHGEDRPGLGENIYKTSVLKFDKNKAAKQASQLWWNELKEFGVGPSNVLTT 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAEKCSEEPSSEEE----NYDVFSAATLNI-----PLEAGNSWWSEIFE------LRG
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                                                                                                                                                                                                                                                                                   23
245 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                245
27308 MW;
                                                                                                                                                                                               14.48; 26.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M., Wolfes H., Raida M., Neumann
                                                                                                                                                                                                                                                                                POTENTIAL:
CYSTEINE-RICH SECRETORY PROTEIN-3.
B93A4E87F402BA22 CRC64;
                                                                                                                                                                                               Score 143.5; DI
Pred. No. 8e-06;
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                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                            Length
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                                                             STITE REPORTED BY SERVICE CONTRACTOR OF STITE STANDARD BY SERVICE 
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   Query Match
                                                                                 SMART; SMO0198; SCP, 1.
SMART; SMO0198; SCP_AG5_PR1_SC7_1; 1.
PROSITE; PS01009; SCP_AG5_PR1_SC7_2; FALSE_NEG.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; FALSE_NEG.
Calcium channel inhibitor; Neurotoxin; Toxin; Signal.
Calcium channel inhibitor; Neurotoxin; Toxin; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDILINE-90260878; PUBMED-1693019;
MCChca-Morales J., Martin B.M., Possani L.D.;
MCChca-Morales J., Martin B.M., Possani L.D.;
MISOLAtion and characterization of helothermine, a novel toxin from
Heloderma horridum horridum (Mexican beaded lizard) venom.";
Toxicon 28:299-309(1990).

Toxicon 28:299-309(1990).

FUNCTION: Toxin that blocks ryanodine receptors. It is toxic to
mice; it causes lethargy, partial paralysis of rear limbs and
lowering of body temperature.

SUBCELLULAR LOCATION: Secreted.

TSUBCELLULAR IOCATION: Secreted.

SIMILARITY: BELONES TO A FAMILY THAT GROUPS MANMALIAN SCP/TPX1;
INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                      InterPro; IPRO01283; Allrgn_V5/Tpx1.
Pfam; pP00188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Morrisette J., Kraetzschmar J., Rendler B., El-Hayek R., Mochca Morales J., Martin B.M., Patel J.R., Moss R.L., Schleuning W.-D., Coronado R., Possani L.D., Moss R.L., "Primary structure and properties of helothermine, a peptide toxin that blocks Tyanodine receptors."; Biophys. J. 68:2280-2288(1995).
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                             SEQUENCE
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TISSUE-Salivary gland;
MEDLINE-95375162; PubMed-7647234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helothermine precursor (HLTx).
Heloderma horridum horridum (Mexican beaded lizard).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     него_негно
Q91055;
                                                                                                                                                                                                                                                                                                                                                              EMBL; U13619; AAC59730.1; -
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Lepidosauria; Squamata; Scleroglossa; Anguimorpha; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 20-39, AND CHARACTERIZATION.
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                                                          20
242 AA;
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27493 MW;
         13.8%;
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      Score 137.5;
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      DB 1;
         Length 242;
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MEDLINE-96270732; PubMed-8665901;
METALINE-96270732; PubMed-8665901;
METALINE-96270732; PubMed-8665901;
METALINE-96270732; PubMed-8665901;
Ponner P., Schleuning W. -D.;
Ponner P., Sc
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01-AGG-1990 (Rel. 15, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Testis-specific protein TPX-1 precursor (Cysteine-rich secretory
InterPro: IPR001283; Allrgn_V5/Tpx1.
Pf4m; PF00188; SCP; 1.
PRINTS; PR00883; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpx1; 1.
                                                                                                                                                                                                                                      EMBL; M25532; AAA61220.1;
EMBL; X95239; CAA64526.1;
PIR; B33329; B33329.
Genew; HGNC:12024; TPX1.
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KESSHARA M., Gutknecht J., Brew K., Spurr N., Goodfellow P.N.;
"Cloning and mapping of a testis-specific gene with sequence
similarity to a sperm-coating glycoprotein gene.";
Genomics 5:527-534(1989).
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                                                                                                                                                                                                      MIM; 187430;
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13; Mismatches 72;
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CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00198; SCP; 1.

PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.

PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.

Testis; Signal; Multigene family.

POTENTIAL.
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                                                                                                                                                                               Kjeldsen L., Cowland J.B., Johnson A.H., Borregeard N.;

*SGP28, a novel matrix glycoprotein in specific granules of human
neutrophils with similarity to a human testis-specific gene product
and a rodent sperm-coating glycoprotein.*;

*FEBS Lett. 380:246-250(1956).

-I- SUBCELJULAR LOCATION: SECRETED; IN NEUTROPHILS, LOCALIZED IN
SPECIFIC GRANULES.

-I- TISSUE SPECIFICITY: SALIVARY GLAND, PANCREAS AND PROSTATE >

-I- TISSUE SPECIFICITY: SALIVARY GLAND, PANCREAS AND PROSTATE >

-EDIDIDYNIS, OVARY, THYMUS AND COLON.

-I- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

INSECTS AG3/AG5; FUNGI SC7/SC14 AND FLANTS PR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRS3_HUMAN STANDARD; PRT; 245 AA.

P54108; O15512;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cysteine-rich secretory protein-3 precursor (CRISP-3) (SGP28 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-96270732; PubMed-8665901;
Kraetzschmar J., Haendler B., Eberspaecher U., Roostermann D.,
Donner P., Schleuning W.-D.;
"The human cysteine-rich secretory protein (CRISP) family. Primary
structure and tissue distribution of CRISP-1, CRISP-2 and CRISP-3.";
Eur. J. Biochem. 236:827-836(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazos; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE-96186934; PubMed-8601434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 YQDLL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 WQNLL 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 NVDVFSAATLNIPLEAGNSWWSEIFELRGKVYNKNGKTSN----IANMVWDSHDKLGCA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENLYMSSDPTSWSSAIQSWYDEILDF---VYGVGPKSPNAVVGHYTQLVWYSTYQVGCG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REIVNK-HNELRKAVSP--PASNMLKMEWSREVTTNAQRWANKCTLQHSDPEDRKTSTRC
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1 21 POTENTIAL.
2 243 TESTIS-SPECIFIC PROTEIN TPX-1.
243 AA; 27259 MW; C5FE698C449CFAD9 CRC64;
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Best Local :
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EMBL; X94223; CAA63984.1; ..
HSSP; P04284; 1CPE.
InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam; PP0018; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
PRODOM; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
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                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurograthi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Testis-specific protein TPX-1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
G1ycoprotein; Signal; Multigene family; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KTSNIANMVWDSHDKLGCAVVDCSG----KTHVVCQYGPEAKGDGKTI--YEEGAPCSRC 160
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239
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N-LINKED (GLCNAC. . .) (POTENTIAL,
S -> P (IN DESNE 195335).
FFIG-VAR_01718
A -> S (IN DESNE 1864312).
FFIG-VAR_011719:
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RESULT 7
VA5_POLDO
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Best Local S
Matches 49
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P8155;
DISULFID
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SEQUENCE
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CHAIN 23 243 T
SEQUENCE 243 AA; 27605 MW;
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PRODOM; PD000542; Allrgn_V5/Tpxl; 1.
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M25533; AAA40472.1; -.
PIR; A33329; A33329
HSSP; P04284; ICFE.
MGD; MGI:98815; Tpx1.
                                                                                                                                                                                                                         ProDom; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00837; V5TPXLIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00188; SCP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001283; Allrgn_V5/Tpx1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE.
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PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:98815; Tpx1.
InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam; PF00188; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             195 NCENGLCTNSCDFEDLL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 GHYTQLVWYSSFKIGCGIAYCPNQDNLKYFYVCHYCPMGNNVMKKSTPYQQGTPCASCPN 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 ----NMVWDSHDKLGCAVVDCSGKTHV----VCQYGPEAKGDGK--TIYEEGAPCSRCSD 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 YGAGVTCDD--DWQNLL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           al Similarity
49; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 EGKDPDFTSLLTNQLQVQREIVNKHNELRRSV--NPTGSDILKMEWSIQATTNAQKWANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 EKLDDDMREMFT-----ELHNGYRAAFARNYKTSKMRTMVYDCTLEEKAYKSAEK 60
    28
172
206 AA;
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104
96
189
         23152 MW;
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    BY SIMILARITY.
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3 CRC64;
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TESTIS-SPECIFIC PROTEIN TPX-1.
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Query Match
Best Local S
Matches 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDILINE-97128816; PubMed-8973356; Rich T., Chen P., Furman F., Huyah N., Israel M.A.; RTVP-1, a novel human gene with sequence similarity to genes of diverse species, is expressed in tumor cell lines of glial but neuronal origin. "; Gene 180:125-130(1996).
   between the the European I use by non-I modified and tentities require
                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 95:2262-2266(1998).

-ITISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE HUMAN BRAIN TUMOR, GLIOBLASTOMA MULTIFORM/ASTROCYTOMA, BUT NEITHER IN NORMAL FETAL OR ADULT BRAIN TISSUE, NOR IN OTHER NERVOUS SYSTEM TUMORS.

-I SIMILARIY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCE/TPX1; INSECTS AG3/AG5; FUNGI SCT/SCI4 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         STRUCTURE BY NMR.

MEDILNE-98151500; PubMed-9482873;

MEDILNE-98151500; PubMed-9482873;

Szyperski T., Fernandez C., Mumenthaler C., Wuethrich K.;

Szyperski T., Fernandez C., Mumenthaler C., Wuethrich K.;

Structure comparison of human glioma pathogenesis-related protein plaa indicates a GlipR and the plant pathogenesis-related protein plaa indicates a functional link between the human immune system and a plant defense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 11-266 FROM N.A.
MEDLINE-95331646; PubMed-7607567;
Murphy E.V., Zhang Y., Zhu W., Biggs J.;
The human glioma pathogenesis-related protein
related to plant pathogenesis-related proteins
expressed specifically in brain tumors.";
Gene 159:131-135(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. TISSUE-Glial tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                              system."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189
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Similarity 23.6%;
6; Conservative 3
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annotation update)
d protein (GliPR) (RTVP-1 protein)
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Pred. No. 0.00049
2; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata;
Catarrhini; Hominidae;
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Best Local S:
Matches 49;
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Pram; PF00188; SCP; 1
PRINTS; PR00887; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpxl; 1.
SMART; SM00198; SCP; 1.
SMART; SS010109; SCP_AG5_PR1_SC7_1; 1
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1
PROSITE; PS01010; PS0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X91911; CAA63005.1;
EMBL; U16307; AAA82731.1;
HSSP; P04284; 1CFE.
MIM; 602692; ..
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01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
sperm-coating 91ycoprotein 1 precursor (SCP 1) (Acidic epididymal 91ycoprotein 1) (Cysteine-rich secretory protein-1) (Crisp-1).
               SEQUENCE FROM N.A.

TISSUE-Submandibular gland;

MEDLINE-93307144; PubMed-8319566;

Haendlar B., Kratzschmar J., Theuring F., Schleuning W.D.;

Haendlar B., Kratzschmar J., Theuring F., Schleuning W.D.;

"Transcripts for cysteine-rich secretory protein-1 (CRISP-1;

"Transcripts for cysteine-rich secretory protein-1 (CRISP-1;

and the novel related CRISP-3 are expressed under androgen co
the mouse salivary gland,";

Endocrinology 133:102-198(1993).

Endocrinology 133:102-198(1993).

FUNCTIONAL MATURATION WHILE THEY MOVE FROM THE TESTIS TO
                                                                                                                                                                                                                                                                                                                                                                TISSUE-Submendibular gland;
MEDLINE-93246016; FubMed-1301383;
MIZUKI N., Kasahara N.;
MIZUKI N., Kasahara N.;
MYOUSE submandibular glands express an androgen-regulated encoding an acidic epididymal glycoprotein-like molecule. epididymal glycoprotein-like molecule. mol. Cell. Endocrinol. 89:25-32(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 DDDMREMFTELHNGYRAAFARNYKTSKMRTMVYDCTLEEKAYKSAEKCS-----EEP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YGAGVTCDDDWQNLLCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NMVWDSHDKLGCAVVDC-----SGKTHVVCQYGPEAKGDGKT-IYEEGAPCSRCSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLHPNFTSLGENIWTGSVPIFSVSS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NDKCLDNLCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCP_AG5_PR1_SC7_1; 1.
SCP_AG5_PR1_SC7_2; 1.
SCP_AG5_PR1_SC7_2; 1.
D -> N (IN REF. 2).
RORDQVKRYYSVYYPGWPIYPRNRYTSLFLIVNSVILILSV
266 RORDQVKRYYSVYYPGWPIYPRNRYTSLFLIVNSVILILSV
1 TIILYQLKYNLLULD -> DSETKSNVTTMLYIRLAHIS
T (IN REF. 2).
1; 30342 MW; C04378085EFB2B7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207
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Pred. No. 0.00074;
0; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; |
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .ch).
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                                      THE TESTIS TO THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   266;
                                                                                                                                                                                                                                                                                                                                                                                                                                            transcript
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50;
                                                                                                                                                                control
                                                                                                                                                                                               DE/AEG)
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197 162 139 87

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VA52_DOLM
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Best Local S
Matches 51
01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
01-JUL-1999 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
venom allergen 5.01 precursor (Antigen 5 form 2) (AG5-2) (Allergen Dol m 5.01) (Dol m V-A).
Dolichovespula meculata (White-face hornet) (Bald-faced hornet).
Dolichovespula meculata (White-face hornet) (Bald-faced hornet).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculata; Vespoldea; Vespoldae; Vespinae; Dolichovespula.
NCBI_TaxID-7441;
                                                                                                                                                                                                                                                                                                                                                                                           DOLMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001283; Aegl.
InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam; PF00188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
PROSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an emmail to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONVOLUTED TUBULES CELLS.

1. TISSUE SPECIFICITY: MAINLY FOUND IN THE CAUDA EPIDIDXMIS WHERE IT IS SYNTHESIZED BY THE PRINCIPAL CELLS AND SECRETED INTO THE LUMEN.
BINDS TO THE HEADS OF SPERMATOZOA. ALSO EXPRESSED IN THE SUBMANDIBULAR GLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M92849; AAA37185.1; -. EMBL; L05559; AAA37460.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -I- DEVELOPMENTAL STAGE: EXPONENTIAL INCREASE BETWEEN DAYS 25 AND 30
                                                                                                                                                                                                                                                                                                                               VA52_DOLMA
P10736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INDUCTION: By androgens.
SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DUCTUS DEFERENS.
SUBCELLULAR LOCATION: STORED IN SECRETORY GRANULES OF GRANULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         164 GAGVTCDDDWQNLLC---IGH 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GHYTQVVWNSTFQVACGVAECPKNPLRYYYVCHYCPVGNYQGRLYTPYTAGEPCASCPDH 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNIANMVWDSHDKLGCAVVDCSG---KTHVVCQYGPEAKGDGK--TIYEEGAPCSRCSDY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KCSEEPSSEE-----ENVDVFSAATLNIPLEAGNSWWSEIFELRGKVYNK--NGKT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----CEDG----LCTNSCGH 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KCTFSHSPIELRTTNLRCGEN--LFMSSYLASWSSAIQGWYNEYKDLTYDVGPKQPDSVV 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSSQENRLEKLSTTKMSVQEEIVSKHNQLRRMVSPS--GSDLLKMEWNYDAQVNAQQWAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145
244 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 SPERM-COATING GLYCOPROTEIN 1
145 N-LINKED (GLCNAC. . .) (POTE)
27679 MW; D00DD0348F85781F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.0%; Score 119.5; DB 1; Length 244; 25.4%; Pred. No. 0.0011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31;
                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                         227 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84; Indels
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RESULT 11
VA5_VESGE
ID VA5_VESGE
AC P35784;
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Best Local S
Matches 39
                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Venom;
MEDLINE-88124947; PubMed-3422469;
MEDLINE-88124947; PubMed-3422469;
Faig K.S.Y., Vitale M., Febliner P., King T.P.;
"CDNA cloning and primary structure of a white-face hornet venom allergen, antigen 5.";
allergen, artigen 5.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-WOV-1997 (Rel. 35, Last annotation update)
Venom allergen 5 (Antigen 5) (A05) (Allergen
Vespula germanica (Yellow Jacket) (Wasp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P04284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; J03601; AAA28301.1; -. PIR; A31085; A31085.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-90384920; PubMed-2402482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venom; Allergen; Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PARTIAL SEQUENCE, AND DISULFIDE BONDS
                                                                                                                                                                                                    110 NIANWVWDSHDKLGCA---VVDCSGKTH-VVCQYGPEAKGDGKTIYE 152
                                                                                                                                                                                                                                   119 FNHDDCRNTAKYQVGQNIAISSTTATQFDRPSKLIKQWEDEVTEFNYKVGLQNSNFRKVG 178
                                                                                                                                                                                                                                                                                                                            13 LDDDMREMFTELHNGYRAAFARNYKT-----SKMRTMVYDCTLEEKAYKSAEKC- 61
                                                                                                                                                                                                                                                                62 -----SEEPSSEEENVDVFS--AATLNIPLEAGNSWWSEIFELRGKVYNKNG----KTS 109
                                                                                                                                                                                                                                                                                             59 LTNDEKNEILKRHNDFRQNVAKGLETRGKPGPQPPAKNMNVLVWNDELAKIAQTWANQCD 118
                                                                                                                                                                                                                                                                                                                                                         1 Similarity
39; Conserv
                                                                                                                                                                        HYTOMVWGKTKEIGCGSIKYIEDNWYTHYLVCNYGPGGNDFNQPIYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR001283; Allrgn_V5/Tpx1
                                                                                                                                                                                                                                                                                                                                                                                                                     54
227 AA;
                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCP;
                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                   54 V
25999 MW;
                                                                                                                                                                                                                                                                                                                                                       11.3%; Score 112.5; DB 1; Length 227; 23.4%; Pred. No. 0.0043; Live 27; Mismatches 74; Indels 27
                                                                                                                                                                                                                                                                                                                                                                                                                                       ٧ ->
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VENOM ALLERGEN 5.01.
                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                   -> A.
4F0ED10D58C44502 CRC64;
                                                                                            204
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                   Ves
                9
                  5) (Yes
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RESULT VARSEULT VARSE
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Best Local S
Matches 39
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SEQUENCE.
SEQUENCE.
TISSUE-Venom;
MEDLIND-94044316; F
"~ffman D.R.;
"~ffman D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antigen 5 molecules and the streativity";

J. Allergy Clin. Immunol. 92:
-!- SIMILARITY: BELONGS TO A
INSECTS AG3/AG5; FUNGI SC
PIR; A44522; A44522
PIR; B44583; B44583
HSSP; P04284; ICFE
                                                                                                                                                                                                                                                                                                                                               01-JUN-1994 (Rel. 29,
01-JUN-1994 (Rel. 29,
16-OCT-2001 (Rel. 40,
Venom allergen 5.02 (
                                                                                                                                                                                                                                                                                                                                                                                                                                  TLT 12
VA52_VESCR
P35782;
MEDITIE=90044116; PubMed=9227862; Hoffman D.R.;

"Allergens in Hymenoptera venom. XXV: T antigen 5 molecules and the structural reactivity.";

J. Allergy Clin. Immunol. 92:707-716(19-1-SIMILARITY: BELONGS TO A FAMILY THA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Venom; Allergen.
DISULFID 4
DISULFID 8
DISULFID 26
DISULFID 170
                                                                                                                                                                                                              Vespa crabro (European hornet),
Eukaryota; Metazoa; Arthropoda; Mandibulata;
Insecta; Pterygota; Neoptera; Endopterygota;
Aculeata; Vespoidea; Vespidae; Vespinae; Vesp
NCBI_TaxID-7445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam; PF00188; SCP: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; P
Insecta; Pterygota; N
Aculeata; Vespoidea;
NCBI_TaxID=30212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    one in Hymenoptera venom. XXV: 7 molecules and the structural
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29, Last sequence update)
40, Last annotation update)
^2 (Antigen 5-2) (AG5-2) (Allergen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed-8227862
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Neoptera; Endopterygota; Hymenoptera; ;
Vespidae; Vespinae; Vespula.
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     92:707-716(1993)
A FAMILY THAT (
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O A FAMILY THAT GRUIN SC7/SC14 AND PLATER
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Pred. No. 0
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Hymenoptera;
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antigenic
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antigenic cros
     MAMMALIAN
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     SCP/TPX1
                                                                                                                                                                                                                                                         Hexapoda,
Apocrita;
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RESULT 13

TPX1_CAVPO STANDARD; PRT; 244

AC 060477;
DT 01.NOV-1997 (Rel. 35, Last sequence upda

REPX1.

OC Cavia porcellus (Guinea pig)

CC Mammalia; Butheria; Rodentia; Hystricogn

OX (REL. TaxID-10141;

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RT SEQUENCE TROM N.A.

RT SEQUENCE OF 22-41.

MO1. Reprod. Dev. 44:221-229(1996).

RN 4EDLINE-88193219; PubMed-328255;

RN 4EDLINE-88193219; PubMed-3282555;

RN 5EQUENCE OF 22-41.

RP 6EQUENCE
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Best Local S
Matches 37
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Pfam; PF00188; SCP; 1.

PRINTS; PR00837; V5TPXLIKE.

ProDom; PD000542; Allrgn_V5/Tpx1; 1.

SMART; SM00198; SCP; 1.

SMART; SM00199; SCP_AG5_PR1_SC7_1; PROSITE; PS01010; SCP_AG5_PR1_SC7_2; PROSITE; PS01010; SCP_AG5_PR1_SC7_2; Venom; Allergen.

DISULED 1 16 BY SIMI DISULED 26 94 BY SIMI DISULED 168 185

DISULED 168 185

SEQUENCE 202 AA; 22781 MW; B7101
     This SWISS-PROT entry is copyright. It is produced through between the Swiss institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                  MEDLINE-88193219; bubmed-3282555;
MEDLINE-88193219; bubmed-3282555;
Hardy D.M., Huang T.T.F. Jr., Driscoll W.J., Tung K.S.K.,
"Purification and characterization of the primary acrosome
autoantigen of guinea pig epididymal spermatozoa.";
Biol. Reprod. 38 423-437(1988).
-!- TISSUE SPECIFICITY: TESTIS.
-!- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN
-! SIMILARITY: BELONGS TO AFAMILY THAT GROUPS MAMMALIAN
-! SIMILARITY: BELONGS TO AFAMILY THAT GROUPS MAMMALIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae;
NCBI_TaxID-10141;
                                                                                                                                                                                                                                                                                                                                                     Foster J.A., Gerton G.L.;
"Autoantigen 1 of the guinea ply sperm acro
mouse Tpx-1 and human TPX1 and is a member
secretory protein (CRISP) family.";
Mol. Reprod. Dev. 44:221-229(1996).
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PIR; H44522; H44522.
PIR; H4453; H44583
HSSP; P04284; 1CFE.
InterPro; IPR001283; Allrgn_V5/Tpx1
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37; Conserv
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SCP_AG5_PR1_SC7_2;
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Pred. No. 0.0046;
4; Mismatches 5
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Jae; Cavía.
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                                                                                                                                           SCP/TPX1;
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RESULT 14
VA5_VESV1
ID VA5_1
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Matches 38
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Interpro; IPR001283; Allrgn_V5/Tpx1.
Pfam; P800188; SCF; 1.
PRINTS; PR00837; V5TPXLIKE.
PRODOM; PB000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCF; 1.
PROSITE; PS01009; SCF_AG5_PR1_SC7_1; 1.
PROSITE; PS01010; SCF_AG5_PR1_SC7_2; 1.
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01-JUN-1994 (Rel. 29, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
venom allergen 5 (Antigen 5) (Ad5) (Allergen Ves vi 5) (Ves vi V).
vespula vidua (Yellow jacket) (Wasp).
Bukaryota; Metazoa; Arthropoda; Mandibulata; Pamcrustacea; Hexapoda
Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
Aculeata; Vespoidea; Vespidae; Vespinae; Vespula.
NCBI_TaxID-30215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and fentities requires a license agreement (See http://www.isb-sib or send an email to license@isb-sib.ch).
                                                                                               PROSITE; PS01009
PROSITE; PS01010
Venom; Allergen.
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P35787;
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                                                                                                                                                                        s; PR00837; V
n; PD000542;
; SM00198; SC
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                                                                                                                                                             SCP; 1.
                                                                                                                   SCP_AG5_PR1_SC7_1;
SCP_AG5_PR1_SC7_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244
27248 MW;
     103
103
189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.1%; Score 111; DE 25.5%; Pred. No. 0.00 tive 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TESTIS-SPECIFIC PROTEIN TPX-1; 58D8DE6EECE16A12 CRC64;
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SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56;
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RESULT 15
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AC P35786;
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Best Local S
Matches 38
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Best Local
                                                                                                                                                                                                                                                                                                                 Venom; ALDISULFID DISULFID DISULFID DISULFID DISULFID SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1; INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
PIR; D44522; D44552.
PIR; D44533; D44533.
HSSP; P04284; 1CFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-VUN-1994 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
venom allergen 5 (Antigen 5) (AG5) (Allergen Ves 5) (Ves
Vespula squamosa (Southern yellow Jacket) (Mag) respecta Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea;
Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Aculeata; Vespoidea; Vespidae; Vespinae; Vespula.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Allergens in Hymenoptera venom. XXV: The amino antigen 5 molecules and the structural basis of reactivity.";
J. Allergy Clin. Immunol. 92:707-716(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00837; V5TPXLIKE.

PRODOM; PD000544; Allrgn_V5/Tpx1; 1.

SMART; SM00198; SCP; 1.

PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.

PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR00128;
Pfam; PF00188; SCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ncureata; Vespoidea;
NCBI_TaxID=30214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-94044316; PubMed-8227862;
114
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                                             102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38;
                                                                                                                                                                                                                           l Similarity
38; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D.R.
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  MVWDSHDKLGCA---VVDCSGKTH-VVCQYGPEAKGDGKTIYE 152
                                             CKDTTKYNVGQNIAV-SSSTAAVYENVGNLVKAWENEVKDFNPTISWEQNEFKKIGHYTQ
                                                                                                                                                                                 REMFTELHNGYRAAFARNYKT-----SKMRTMYYDCTLEEKAYKSAEKC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --EEPSSEEENVDV-----FSAATLNIPLEAGNSWWSEIFELRGKV-YNKNG--KTS
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                                                                                        --SEEPSSEEENVDVFSAATLNIPLEAGN---SWWSEIFELRGKV---YNKNGKTSNIAN
                                                                                                                                      KQEILKIHNDERNKVARGLETRGNPGPQPPAKNMNNLVWNNELANIAQIWASQCKYGHDT
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                                                                                                                                                                                                                                                                                                                    205 AA;
                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                 17 E
102 E
95 E
188 E
23114 MW;
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22.6%; Pred. No. 0.00
Live 31; Mismatches
                                                                                                                                                                                                                           29;
                                                                                                                                                                                                                         Score 108.5;
Pred. No. 0.00
29; Mismatches
                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                           J.0086;
67;
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es 72; Indels
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antigenic cross-
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                                                                                                                                                                                                                                                                         205;
                                                                                                                                                                                                                           29;
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Apocrita;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153
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                                                                                                                                                                                                                              Gaps
                                             160
                                                                                           113
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161

MVWAKTKEIGCGSIKYVDNNWYTHYLVCNYGPAGNFGNQEVYE 203

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VA53_DOLMA

ID VA53_DOLMA

ID VA53_DOLMA

RC P10737;

AC P10737;

DT 01-UUL-1989 (Rel. 11, Created)

DT 01-UN-1994 (Rel. 29, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Venom allergen 5.02 precursor (Antigen 5 form 3) (AG5-3) (Allergen Dol DE m 5.02) (Dol m V-B) (Fragment).

DE m 5.02) (Dol m V-B) (Fragment).

OS DO11chovespula maculata (White-face hornet) (Bald-faced hornet).

OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

OC Insecta; Pterygota; Neoptera; Endoptarygota; Hymenoptera; Apocrita;

OC Aculeata; Vespoidea; Vespidae; Vespinae; Dol1chovespula.
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Best Local S
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         King T.P., Moran D., Wang D.F., Rochoumian L., Chait B.T.;
"Structural studies of a hornet venom allergen antigen 5, Dol m V and
its sequence similarity with other proteins.";
protein Seq. Data Anal. 3:263-266(1990).
-i- SIMILARITY: BELONGS TO A FAMILY THAY GROUPS MANMALIAN SCP/TPX1;
INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; J03602; AAA28302.1; ALT_TERM. PIR; B31085; B31085.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIINE-88124947; PubMed-3422469;
Fang K.S.Y., Vitale M., Fehlner P., King T.P.;
"CDNR cloning and parimary structure of a white-face hornet venom
allergen, antigen 5.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PARTIAL SEQUENCE, AND DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pro; IPR001283; Allrgn_V5/Tpx1. PF00188; SCP; 1.
                                          63
                                                                                                       46
                                                                                                                                                            13 LDDDMREMFTELHNGYRAAFARNYKT-----SKMRTMVYDCTLEEKAYKSAEKCS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; PD000542; Allrgn_V5/Tpx1; 1.
SM00198; SCP; 1.
                                                                                                                                                                                                                                     40;
                                                                                                                                                                                                                                                                Similarity
------EPPSSEEENVDVFSA-----ATLNIPLEAGNSWWSEIFEL----RGKVYNKN- 105
                                                                                               VSNDEKNEIVNRHNQFRQKVAKGLETRGNPGPQPPAKNMNVLVWNDELAKIAQTWANQCS 105
                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                   24270 MW;
                                                                                                                                                                                                                                                                10.8%; Score 108; 23.4%; Pred. No. 0.
                                                                                                                                                                                                                                 30; M1smatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VENOM ALLERGEN 5.02.
                                                                                                                                                                                                                                                                                                                                                               D8FEEBE99CE9A0BA CRC64;
                                                                                                                                                                                                                                                            DB 1; Length 215;
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RESULT 18
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CRVP_TRIMU
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Best Local
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1- FUNCTION: May be a toxin that blocks ryanodine receptors.

1- SUBCELLULAR LOCATION: Secreted.

1- TISSUE SPECIFICITY: Produced by the venomous gland.

1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
Calcium channel inhibitor; Neuropoxia; Toxin; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Venom gland;
MEDLINE-97385768; PubMed-9241782;
Chang T.-Y., Mao S.-H., Guo Y.-W.;
"Cloning and expression of a cysteine-rich venom protein from "Timeresurus mucrosquamatus (Taiwan habu).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Czeated)
01-NOV-1997 (Rel. 35, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Cysteine-rich venom protein precursor (CRVP).
Trimeresurus mucrosquamatus (Taivan habu)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U59447; AAB48565.1; -.
InterPro; IPR001283; Allrgn_V5/Tpx1.
                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00188; SCP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Protobothrops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-103944;
                                                          131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 GKTSNIANMYWDSHDKLGCA---VVDCSGKTH-VVCQYGPEAKGDGKTIYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 FGHDQCRNTEKYQVGQNVAIASTTGNSYATMSKLIE---MWENEVKDFNPKKGTMGDNNF 162
                                                                                                                                                                             104 KNGKTSNIANMVWDSHDKLGCAVVDCSGKTH---VVCQYGPEAKGDGKTI--YEEGAPCS 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 SKVGHYTQMVWGKTKEIGCGSVKYIENNWHTHYLVCNYGPAGNYMDQPIYE 213
                                                                                                                                                                                                                                                                                                     38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SM00198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PR00837; V5TPXLIKE.
PD000542; Allrgn_V5/Tpx1; 1.
SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                        Similarity
                                                             -----DCPSDCDNGLC 141
                                                                                                RCSDYGAGVTCDDDWQNLLC 178
                                                                                                                                      SNAATGHYTQIVWYKSYRGGCAAAYCPSSKYRYFYVCQYCPAGNMIGKTATPYTSGPPCG 130
                                                                                                                                                                                                                   AERWAYRCIESHSSRDSRVIGGIKCGENIYMSPYPAKWTDIIHAWHGEYKDFKYGVGAVP 70
                                                                                                                                                                                                                                                         AYKSAEKCSEEPSSEEENVDVFSAATLNIPLEAGNSWWSEIF-----ELRGKVYN----- 103
                                                                                                                                                                                                                                                                                                                                                                                 183 AA;
                                                                                                                                                                                                                                                                                              10.7%; Score 107; DB 1; Length 183; ilarity 27.1%; Pred. No. 0.01; Conservative 12; Mismatches 66. There
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                                                                                                                                                                                                                                                                                                                                                                              20378 MW;
                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
CYSTEINE-RICH VENOM PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                 50224D8E92A64930 CRC64;
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VA5_VESMO
ID VA5_VESMO
DT O1.JU
DT 01.JU
DT 01.WO
DE Vesnom
OS Vespu
OC ELKAI
OC ACLLÉ
OX NCBL,
RN (1)
RN (2)
RN (
   RR RR R OCCOCC SET TO ACC
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Best Local S
Matches 38
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HSSP; P04284; ICFE:
InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam; PF00188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
PRODOM; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
PROSITE; PS01001; SCP_AG5_PR1_SC7_2; 1.
                                                                                                                           01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1997 (Rel. 35, Last annotation update)
01-MOV-1997 (Rel. 35, Last annotation update)
venom allergen 5 (Antigen 5) (AG5) (Allergen Ves f 5) (Ves
Vespula flavopilosa (Yellow Jacket) (Wasp)
Euxaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea;
Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Aculeata; Vespoldae; Vespidae; Vespinae; Vespula.
NCBI_TaxID-30211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-93203603; PubMed-8454859;
Lu G. Villalba M., Coscia M.R., Hoffman D.R., King T.P.;
Sequence analysis and antiqenic cross-reactivity of a venom
allergen, antigen 5, from hornets, wasps, and yellow jackets.";
J. Immunol. 150:2823-2830(1993);
1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
PIR, B37329; B37329.
RISPP, B47329; B37329.
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01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1997 (Rel. 35, Last sequence update)
01-NUV-1997 (Rel. 35, Last annotation update)
venom allergen 5 (Antigen 5) (AG5) (Allergen Ves m 5) (Ves m V).
Vespula maculifrons (Eastern yellow Jacket) (Wasp).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
Aculeata; Vespoidea; Vespidae; Vespinae; Vespula.
                                                                                                                                                                                                                                                                                                                                                                                  VA5_VESFL
P35783;
MEDLINE-94044316;
Hoffman D.R.;
                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SENNFLKIGHYTQMVWANTKEVGCGSIKYIQENWHKHYLVCNYGPSGNFQNEELYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NKNG--KTSNIANMVWDSHDKLGCA----VVDCSGKTHVVCQYGPEAKGDGKTIYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQVWANQCQYGHDTCRDVAKYQVGQNVALTGSTAAVYNDPVKLVKMWEDEVKDYNPKKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AYKSAEKC-----SEEPSSEEENVDVFSAATLNIPLEAGNSWWSEIFELR-GKVY 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YGLTKQEKQ--DILKE-----HNDFRQKIARGLETRGNPGPQPPAKNMKNLVWSDELAYI
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170
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2 101
2 94
187
23332 MW;
                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                            PubMed=8227862;
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Pred. No. 0.01
34; Mismatches
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                                                                                                                                                                                       Pancrustacea; Hexapoda;
Hymenoptera; Apocrita;
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                                                                                                                                                                                                                                                                      f 5) (Ves f V).
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VA51_VESCR
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Best Local S
Matches 38
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DISULFID
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                   Vespa crabro (European hornet).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Aculeata; Vespoidea; Vespidae; Vespinae; Vespa.
NCBI_TaxID-7445;
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PRODOM; PRO000542; Allrgn_V5/Tpx1; 1.

SMART; SM00198; SCP; 1.

PROSITE; PS01009; SCP_AG5_PR1_SC7_1;

PROSITE; PS01010; SCP_AG5_PR1_SC7_2;
                                                                                                                                                                                              MEDLINE-94044316; PubMed-8227862;
Hoffman D.R.;
*Allergens in Hymenoptera venom. XXV: The amino antigen 5 molecules and the structural basis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001283; Allrgn_V5/Tpx1 Pfam; PF00188; SCP; 1....
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                                 HSSP; P04284;
InterPro; IPR
                                                                                                                                                                                                                                                                                                    SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NKNG--KTSNIANMVWDSHDKLGCA----VVDCSGKTHVVCQYGPEAKGDGKTIYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YGLTKQEKQ--DILKE-----HNDFRQKIARGLETRGNPGPQPPAKNMKNLVWNDELAYV 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGNNFLKTGHYTQMVWANTKEVGCGS IKF IQEKWHKHYLVCNYGPSGNFQNEELYQ
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                   IPR001283; Allrgn_V5/Tpx1
188; SCP; 1.
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26
170
204 AA;
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101 B:
94 B:
187 B:
23274 MW;
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21.6%; Pred. No. 0.01
tive 35; Mismatches
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                                                                                                                                                                                                  acid sequences of antigenic cross.
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                                                                                                                                         SCP/TPX1;
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Query Match
Best Local Similarity
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SMART; S
                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use of the profit of the statement is not removed. It is not way modified and this fatherent is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                             Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
SubmitARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
Eukaryota; Metazoa; Rematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created).
01-NOV-1997 (Rel. 35, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical 35.0 kDa protein F48E8.1 in chromosome
F48E8.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
                                                                                                 PROSITE;
                                                                                                                     Wormbep; F4888 1, CE01953.
InterPro; IPR001283; Allryn_V5/Tpx1.
Pfam; PF00188; SCP; 1.
PRINTS; PR00837; V5TPXIIKE.
PRODOM; PD000542; Allryn_V5/Tpx1; 1.
SMART; SN00198; SCP; 1.
                                                                    Hypothetical
DOMAIN 2
                                                                                                                                                                                             EMBL; U23514; AAC46538.1; -. WormPep; F48E8.1; CE01953.
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 HDKLGCAVVDC--SG--KTHVVCQYGPEAKGDGKTIYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 SVGQNIAEGSTTADNFGSVSNMVKM-----WEDEVKDYQYGSPKNKLNKVGHYTQMVWAK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SM00198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . Similarity
35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PD000542; Allrgn_V5/Tpx1; 1.
SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TKEIGCGSIKYIENGWHRHYLVCNYGPAGNVGNEPIYE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---EEPSSEEENVDVFSAATLNIPLEAGNSWWSEIFELR-GKVYNKNGKTSNIANMVWDS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HNEFROKVARGLETRGNPGPOPPAKSMNTLYWNDELAQIAQVWANQCNYGHDNCRNSAKY 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HNGYRAAFARNYKT------SKMRTMVYDCTLEEKAYKSAEKCS------
                                                                                             PS01009; SCP_AG5_PR1_SC7_1; FALSE_NEG.
PS01010; SCP_AG5_PR1_SC7_2; FALSE_NEG.
                                          299
312 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                     1 protein.
265 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22722 MW;
                                            35054 MW;
   10.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.6%; Score 105.5; DB 1; 22.2%; Pred. No. 0.016; tive 26; Mismatches 62;
                                                        POLY-THR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
CHORDS 19905B598997 CRC64;
 Score 105; DB 1;
Pred. No. 0.029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                            AEFC7BFF25E26288 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    312 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62; Indels
                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    III.
                  312;
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VAS_VESPE

IDS VAS_V

AC P3578

AC P3578

AC P3578

DT 01-JU

DT 01-JU

DT 01-JU

DT 01-JU

DT 01-W

OC Enkar

OC Acuse

OC Acuse

OC Acuse

OC Acuse

INSECUTE

RA 1550

RA 1515

RA HOFFM

DA HOFFM

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DA SHART

DA SHAR
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Best Local S
Matches 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
venom allergen 5 (Antigen 5) (AG5) (Allergen Ves p 5) (Ves p V).
Vespula pensylvanica (Western yellow Jacket) (Wasp).
Eukaryota: Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
Aculeata; Vespoidas; Vespidae; Vespinae; Vespula.
NCBI_TaxID-30213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VA5_VESPE
P35785;
                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reactivity,";
J. Allergy Ciin. Immunol. 92:707-716(1993).
-I- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
-INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
PIR; C44522; C44523.
PIR; C44533; C4453.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-94044316; PubMed-8227862;
Hoffman D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO0837; V5TPXLIKE.

PROD00542; Allrgn_V5/Tpx1; 1.

SMART; SM00198; SCP; 1.

PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.

PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Allergens in Hymenoptera venom. XXV: The amino acid sequences of antigen 5 molecules and the structural basis of antigenic cross-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nterPro; IPR001283; Allrgn_V5/Tpx1.fam; PF00188; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSP; P04284; 1CFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152 EEGAPCSRC 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 KTNLYGCGFSRCRDVQGVWGRGHRNVFVCHYNPQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 SHDKLGCAVVDCS-----GKTH---VVCQYGPEAKGDGKTIY------------- 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 CDFRHSRGRINVGENIWAAPYSNYS-DAISIWFNEVHNPRCGCNHAYKHCCGHYVQVVWA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               235 GDNGKCSNC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
      107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 QSDSGLLSRSEHPNEYLKKWITHEHNRYR----RMVPASDMNMLYWSDELAASAQRHADT 119
                                                   93
                                                                                                       60
                                                                                                                                                        38
                                                                                                                                                                                                           10 REKLDDDMREMFTELHNGYRAAFARNYKT-----SKMRTMVYDCTLEEKAYKSAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EGDYSLCOOREKLDDDMREMFTELHNGYRAAFARNYKTSKMRTMYYDCTLEEKAYKSAEK
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                                                                                                                                                                                                                                                               Similarity 20.6
35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CSEEPSSEEENV--DYFSAATLNIPLEAGNSWWSEIFELR-GKYYNKNGKTSNIANMVWD 117
                                                                                                                                                           KEEKQDILKE-----HNDFRQKIARGLETRGNPGPQPPAKNMKNLVWNDELAYVAQVWAN 92
      KTSNIANMVWDSHDKLGCAVVDCS----GKTHVVCQYGPEAKGDGKTIYE
                                                       QCQYGHDTCRDVAKYPVGQNVALTGSTADKYDNPVKLVKMWEDEVKDYNPKKKFSENNFN
                                                                                                       KC-----SEEPSSEEENVDVFSAATLNIPLEAGNSWWSEIFELRGK---VYNKNG 106
                                                                                                                                                                                                                                                                                                                                                                       26
170
204 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                       17
101
94
187
187
23317 MW;
                                                                                                                                                                                                                                                                                            10.3%;
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                                                                                                                                                                                                                                                                      31;
                                                                                                                                                                                                                                                                  Score 103; DB Pred. No. 0.02 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204
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                                                                                                                                                                                                                                                                                            DB 1; Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; 08
                                                                                                                                                                                                                                                                      72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -GNTVFVTARGQLYAMPAFTWAS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                      32;
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60
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153

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Query Match
Best Local S
Matches 39
                                                                                                                                                                                                                   **SAMART: $MO0198; $CFP; 1.**
**SAMART: $MO0198; $CFP; 1.**
**PROSITE; PSO10109; $CFP_AG5_PR1_SC7_2; 1.**
**PROSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDILINE-93203603; PubMed-8454859;
Lu G., Villalba M., Coscia M.R., Hoffman D.R., King T.P.;
"Sequence analysis and antigenic cross-reactivity of a venom
allergen, antigen 5, from hornets, wasps, and yellow jackets.";
J. Immunol. 150:2823-2830(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M98858; AAA30333.1; -.
EMBL; A738849; CAB42887.1; -.
HSSP; P04284; ICFE
InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam; PF00188; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vespula vulgaris (Yellow jacket) (Wasp).
Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea;
Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; F
Aculeata; Vespoidea; Vespidae; Vespinae; Vespula.
NCBI_TaxID=7454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0837; V5TPXLIKE.
PRODOM; PD000542; Allrgn_V5/Tpx1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.,
                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KIGHYTQMVWANTKEIGCGSIKYIQNEWHKHYLVCNYGPSGNFGNEELYQ
                                   YSLCQQREKLDDDMREMFTELHNGYRAAFARNYKT----SKMRTMYYDCTLEEK
      YGLTKQEKQ -- DILKE----
                                                                                                                Conservative
                                                                                                                                                                                                          23
227
40
114
117
210
210
119
119
113
219
25798 1
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                                                                                                                32;
                                                                                                                                                                                                                   VENOM ALLERGEN 5.

BY SIMILARITY.

BY SIMILARI
                                                                                                             Score 103; DB
Pred. No. 0.03
32; Mismatches
      -HNDFROKIARGLETRGNPGPQPPAKNMKNLVWNDELAYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence from the venom allergen
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                                                                                                                                         .03;
                                                                                                                                                                1;
                                                                                                                                                             Length
                                                                                                                                                                                                                      CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAMMALIAN SCP/TPX1;
                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ves v 5) (Ves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Hexapoda;
Apocrita;
                                                                                                                44;
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                                                                                                             Gaps
      100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEG2_MOUSE
                                                                                                                PIR;
                                                                                                                                                                EMBL; M92850; AAA37186.1;
EMBL; L05560; AAA37461.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Submandibular gland;
MEDLINE-93246016; PubMed-1301383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AFTER BIRTH.
INDUCTION: BY
SIMILARITY: 1
                                                                                                             B49202; B49;
MGI:102552;
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II:102552; Aeg2.
ro; IPR001283; A
PF00188; SCP; 1.
PR00837; VSTPX
PD0000542; Allr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q 225
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   Allrgn_V5/Tpx1;
                                                                                   Allrgn_V5/Tpx1
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01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
15-7UN-2002 (Rel. 41, Last annotation update)
15-7UN-2002 (Rel. 41, Last annotation update)
Sperm-coating glycoprotein 2 precursor (SCP 2) (Acidic epididymal glycoprotein 2) (Cysteine-rich secretory protein-3) (Crisp-3)
AEG2 OR AEG-2.
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          DUCTUS DEFERENCE.

-1- SUBCELLULAR LOCATION: STORED IN SECRETORY
-1- TISSUE SPECIFICITY: EXPRESSED IN SUBMANDIB
-1- TISSUE SPECIFICITY: EXPRESSED IN SUBMANDIB
-1- DEVELOPMENTAL STAGE: EXPONENTIAL INCREASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Submandibular gland;
MEDLINE-93307144; PubMed-831956;
Haendler B, Kratzschmar J., Theuring F., Schleuning W.D.;
Haendler B, Kratzschmar J., Theuring F., Schleuning W.D.;
*Transcripts for cysteine-rich secretory protein-1 (CRISP-1; DE/ABG)
and the novel related CRISP-3 are expressed under androgen control in
the mouse salivary gland.";
Endocrinology 133:192-198(1993).
1- FUNCTION: THIS PROTEIN IS SUPPOSED TO HELP SPERMATOZOA UNDERGO
FUNCTION: THIS PROTEIN IS SUPPOSED TO HELP SPERMATOZOA UNDERGO
FUNCTION: THIS PROTEIN IS SUPPOSED TO HELP SPERMATOZOA UNDERGO
FUNCTION: THIS PROTEIN IS SUPPOSED TO HELP SPERMATOZOA UNDERGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mulzuki N., Kasahara M.;

Musue submandibular glands express an androgen-regulated transcript encoding an acidic epididymal glycoprotein-like molecule.";

Mol. Cell. Endocrinol. 89:25-32(1992).
                                                                                                                                                                                                                                                                                                                    INDUCTION: By androgens.
SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN
INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PKKKFSGNDFLKTGHYTQMVWANTKEVGCGSIKYIQEKWHKHYLVCNYGPSGNFMNEELY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBMANDIBULAR GLAND.
INCREASE BETWEEN DAYS 25
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                                 EMBL; M98859; AAA28303.1; -.
HSSP; P04284; ICFE.
InterPro, IPR001283; Allrgn_V5/Tpx1.
Pfam; PP00188; SCP; 1.
PFANTS; PR00337; V5TPXLIKE.
PTDDOM; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Venom allergen 5 (Antigen 5) (AG5) (Allergen Dol a 5) (Dol a V).
Politchovespula arenaria (Yellow hornet)
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
Aculeata; Vespoidea; Vespidae; Vespinae; Dolichovespula.
NCBI_TaxID-7442;
PROSITE; PS01009; SCP_AG5_PR1_SC7_1; PROSITE; PS01010; SCP_AG5_PR1_SC7_2;
                                                                                                                                                                                                                                                                                                                                                                                Lu G., Villalba M., Coscia M.R., Hoffman D.R., King T.P.;
"Sequence analysis and antigenic cross-reactivity of a venom
allergen, antigen 5, from hornets, wasps, and yellow jackets.";
J. Immunol. 150:2823-2830(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-93203603; PubMed-8454859;
Lu G., Villalba M., Coscia M.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VA5_DOLAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1; INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 SCPD----RCED 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 RCSDYGAGVTCDD 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 VGHHTQVVWKSNLQVACGVAECPENPLRYFYVCRYCPVLNYSGHYPSRPYLAYTARAPCA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 -----NNVWDSHDKLGCAVVDCSG---KTHVVCQYGPEAKGDGK-----TIYEEGAPCS 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87 IELRTINLKCGEN--LEMSSYL-VP-----WSSVIQGWYNESKGLIFGV-GPKQNVSV 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 EE-----ENVDVFSAATLNIPLEAGNSWWSEIF----ELRGKVYNKNGKTSNIA- 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 EKLDDDMREMFTEL -- - HNGYRAAFARNYKTSKMRTMVYDCTLEEKAYKSAEKCSEEPSS 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 EKLSTSKKSVQEEIVSKHNQLRKVSPS--GSDLLNMEWNYDAQVNAQQRADKCTFSHSP 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 SP
118 N-
132 N-
175 N-
; 27314 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.1%; Score 101; DB 1; Length 241; 23.3%; Pred. No. 0.049;
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N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

LINKED (GLCNAC. .) (POTENTIAL).
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RESULT 26
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ID PRIA_LY
AC Q08697
DT 01-OCT
DT 01-OCT
DT 15-JUN
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OS LYCOPE
OC EMARY
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DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-CV. Rutgers; TISSUE-Leaf;

MEDLINE-94447356; PubMed-8190070;

Tornero P. Conejero V. Vera P.;

Tornero P. Conejero V. Vera P.;

A gene encoding a novel isoform of the PR-1 protein family from tomato 1s induced upon viroid infection.";

MOI. Gen. Genet. 243:47-53(1994)

1. FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS

ACAINST PATHOCENS (BY SIMILARITY).

1. INDUCTION: SYNTHESIZED DURING PATHOGEN INFECTION OR OTHER STRESS-

1. SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

INSECTS AG3/AG5; FUNGI SCT/SC14 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIA_LYCES STANDARD; PRT; 175 AA.

008697;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pathogenesis-related protein 1Al precursor (PR-1A1).
Lycopersicon esculentum (Tomato).
Lycopersicon esculentum (Tomato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

NCBI_TaxID-4081;
Interpr: IPRO01283; Allrgn_v5/Tpx1.
Pf4m; PF00188; SCP; 1.
PRINTS; PR000837; VSTPXLIKE.
PRODOM; PD000542; Allrgn_v5/Tpx1; 1.
SMART; SM00198; SCP; 1.
PR0SITE; PS01100; SCP_AG5_PR1_SC7_1;
PR0SITE; PS011010; SCP_AG5_PR1_SC7_2;
                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                     EMBL; X71592; CAA50596.1; -. HSSP; P04284; ICFE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 GPEAKGDGKTIYE 152
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37; Conser
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169
203 AA;
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23202 MW;
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19.2%; Pred. No. 0.044;
Live 31; Mismatches
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Query Match
Best Local
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         TISSUE-Venom;

MEDLINE-90285439; PubMed-2355158;

HOffman D.R., Smith A.M., Schmidt M., Moffitt J.E., Guralnick M.,

*Allergens in Hymenoptera venom. XXII. Comparison of venoms from t

species of imported fire ants, Solenopsis invicta and richteri.*;

J. Allergy Clin. Immunol. 85:988-996(1990).

1. DISEASE: THE MOST COMMON CAUSE OF INSECT VENOM ALLERGY IN THE

SOUTHEASTERN QUITED STATES IS THE IMPORTED FIRE ANT.

1. SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MANMALIAN SCP/TPX.

INSECTS AG3/AG5; FUNGI SCT/SC14 AND PLANTS PR-1.
 This SWI
between
                                                                                                                                                                                                                                                                                                                                 93778; O16135; Q9Twzz;
93778; O16135; Q9Twzz;
01-JUN-1994 (Rel. 29, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Venom allergen III precursor (Allergen Sol 1 3) (Sol 1 III).
Solenopsis invicta (Red imported fire ant).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
Aculeata; Formicidae; Myrmicinae; Solenopsis.
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                                                                                                                                                                                                                                                                                          TISSUE-Venom;
Hoffman D.R., Farrar D., Schmidt M., McConnell T.J.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                         VA3_SOLIN
P35778; 01
                                                                                                                               PARTIAL
                                                                                                                                                                                        Hoffman D.R.
                                                                                                                                                                                                 MEDLINE-93139387; PubMed-8423273;
                                                                                                                                                                                                                    SEQUENCE OF 23-234
                                                                                                                                                                                                                                        Allergy
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                                                                                                                                                                   Allergens in Hymenoptera venom XXIV: the amino acid sequences imported fire ant venom allergens Sol i II, Sol i III, and Sol
                                                                                                                                                                                                           FISSUE-Venom
                                                                                                                                                                                                                                      "Fire ant venom allergy.";
Allergy 50:535-544(1995).
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                Allergy Clin.
SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
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                                      MAMMALIAN SCP/TPX1;
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01-JUN-1994 (Rel. 29, Created)
15-JUN-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Venom allergen III (Allergen Sol r 3) (Sol r III).
Solenopais richteri (Black imported fire ant).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea;
Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Aculeata, Formicidae; Myrmicinae; Solenopais.
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HOFfman D.R., Smith A.M., Schmidt M., Moffitt J.E., Guralnick M.; Rallergens in Hymenoptera venom. XXII. Comparison of venoms from "Rallergens of imported fire ants, Solenopsis invicta and richteri.", species of imported fire ants, Solenopsis invicta and richteri.", Allergy Clin. Immunol. 85:988-996(1990).
J. Allergy Clin. Immunol. 85:988-996(1990).
                                                                                                                                                       SEQUENCE OF 1-20.
MEDLINE-90285439;
Hoffman D.R., Smit
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE.
SEQUENCE.
MEDLINE-98049167; PubMed-9389299;
Hoffman D.R.;
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PIR; C44582; C44582.
HSSP; P04284; 1CFE.
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S; PR00837; V
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PD000542; Allrgn_V5/Tpx1;
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)188; SCP; 1.
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Pred. No. 0.13
23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211
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0.13;
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RESULT
VA5_POI
            ACCOCCATE FIT NOR DESCRIPTION OF THE FIT NOR DES
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Best Local
         DISULFID
DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-NUN-1997 (Rel. 35, Last annotation update)
Venom allergen 5 (Antigen 5) (AG5) (Allergen Pol f 5) (Pol f V).
Polistes fuscatus (Paper wasp).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidaa; Vespidae; Polistinae; Polistes.
NCBI_TaxID-30207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLFU
                                                                                                                                                                                                                                                                                                                                                                     -I- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMM
INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
PIR; F44522; F44583
PIR; F44583; F44583
HSSP; P04284; 1CFE.
                                                                                                                           DISULFID
                                                                                                                                                                                                                                      SMART;
                                                                                                                                                                     PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Allergy Clin. Immunol. 92:707-716(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94044316; PubMed=8227862; Hoffman D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00837; V5TPXLIKE.
Probom; P0000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
SMART; SM00198; SCP_AG5_PR1_SC7_1; 1.
PROSITE; PS01009; SCP_AG5_PR1_SC7_2; 1.
                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001283; Allrgn_V5/Tpx1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *Allergens in Hymenoptera venom. XXV: The amino acid sequences cantigen 5 molecules and the structural basis of antigenic cross-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLFU
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                                                                                                                                                                                                                                                                                                                 PF00188; SCP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      152 SDGNILMHVGHYTQIVWAKTKKIGCGRIMFKEDNWNKHYLVCNYGPAGNVLGAQIYE 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 KTSNI-----ANMYWDSHDKLGCAVV----DCSGKTHVVCQYGPEAKGDGKTIYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 HDACRNVERFAVGQNIAATSSSGKNKSTLSDMIL-----LWYNEVKDFDNRWISSFP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pro; IPR001283; Allrgn_V5/Tpx1
PF00188; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52
                                                                                                                                                                                                                                      SM00198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Allergen.
DE 211 AA; 23869 MW; 99683BBA72844E9B CRC64;
                                                                                                                                                                                                                   PRO0837; V5TPXLIKE.
PD000542; Allrgn_V5/Tpxl; 1.
SM00198; SCP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DAEKDAIVNKHNELRORVASGKEMRGTNGPOPPAVKMPNLTWDPELATIAORWANOCTFE 99
         205 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.6%; Score 95.5; DB
ilarity 21.5%; Pred. No. 0.13;
Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                             16
104
96
            23068 MW;
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BY SIMILARITY.
77308250FBBF2357 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GROUPS MAMMALIAN SCP/TPX1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71; Indels 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAMMALIAN SCP/TPX1;
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RESULT
YJH9_YE
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Best Local :
  PRINTS; PRO0837; V5TPXLIKE.

PRODOM: PD000542; AllIGn_V5/Tpx1; 1.

SMART; SM00198; SCP_AG5_PR1_SC7_1; 1.

PROSITE; PS01009; SCP_AG5_PR1_SC7_2; 1.

PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.

Hypothetical protein; Signal.

SIGNAL

1 19 POTENTIAL.

CHAIN 20 299 HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                        EMBL; 249354; CAA89372.1; -.
EMBL; X83502; CAA58491.1; -.
EMBL; X88851; CAA61315.1; -.
HSSP; P04284; LCFE.
SGD; S0003615; YJL079C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Sequence analysis of a 33.1 kb fragment from the left arm of Saccharomyces cerevisiae chromosome X, including putative proteins with leucine zippers, a fungal Zn(II)2-Cys6 binuclear cluster domain and a putative alpha 2-SCB-alpha 2 binding site."; Yeast 11:681-689(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             precursor.
YJL079C OR J1022.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical 30.6 kDa protein in SCP160-SNC3
                                                                                                                                                   InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam; PF00188; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-96093911; PubMed-7483841;
Miosga T., Schaaff-Gerstenschlaeger I., Chalwatzis N., Ba
Boles E., Fournier C., Schmitt S., Veiten C., Wilhelm N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Asacomycota; Saccharomycetina; Saccharomycetales; Saccharomycetaceae; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YJH9_YEAST
P47032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MANMALIAN SCP/TPX1; INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 VCQYGPEAKGDGKTIY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 LIKLWENEVKDFN---YNKGITKQNFGKVGHYTQMIWAKTKEIGCGSLKYMKNNMQHHYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 ----WWSEIFELRGKVYNKN-----GKTSNIANMVWDSHDKLGCAVVDCSGKT----HV 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 PAASDMNNLVWNDELAHIAQVWASQCQILVHDKCRNTAKYQVGQ-NIAYAGGSKLPDVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 ---SKMRTMVYDCTLEEKAYKSAEKCSEEPSSEEENVDVFSAATLNIPLEAGNS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 GIHTVCQYGESTKPSKNCADKVIKSVGPTEEEKKLIVNEHNRFRQKVAQGLETRGNPGPQ 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GDYSLCQQREKL-------DDDMREMFTELHNGYRAAFARNYKT------
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POTENTIAL.
HYPOTHETICAL PROTEIN YJL079C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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Best Local S
Matches 36
                                                  Matches
                                                                   Query Match
Best Local
                                                                                                                                         DISULFID DISULFID SEQUENCE
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Q41359;
01-NOV-1997
01-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pathogenesis-related protein PR-1 type precursor.
Sambucus nigra (European elder).
Eukaryota; VIridiplantae; Streptophyta; Embryophyta; Tracheo
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Dipsacales; Adoxaceae; Sambucus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
SEQUENCE
                                                                                                                                                                   PROSITE; PS01009; SCP_AGS_PRI_SC7_1; 1.

PROSITE; PS01010; SCP_AGS_PRI_SC7_2; 1.

Plant defense; Pathogenesis-related protein; Signal.

SIGNAL:

CHALN

30 167

PATHOGENESIS-RELATED PROBLEMENT PROBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z46947; CAA87071.1; -. HSSP; P04284; ICFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPXI: INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Abscission zone;
Coupe S.A., Taylor J.E., Roberts J.A.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF AGAINST PATHOGENS.
                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00198;
                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam; PF00188; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD000542; Allrgn_V5/Tpx1;
                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00837; V5TPXLIKE
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                                               1 Similarity
42; Conserv
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llarity 23.2%;
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30634 MW;
                                                                                                                                            18410 MW;
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                                            ; Score 94.5; DB 1; ; Pred. No. 0.12; 18; Mismatches 50;
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                                                                                                                                         PATHOGENESIS-RELATED PROTEIN PR-1 TYPE. BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
37 SIMILARITY.
472BAB3269592E53 CRC64;
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; A316769CA87C5679 CRC64;
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  ----AAFARNYKTSKMRTMVYDCT 49
                                               50;
                                                                                            Length 167;
                                               Indels
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A Yoshida M.C., Kirchhoff C., Ishibashi T., Kasahara M.;
A Yoshida M.C., Kirchhoff C., Ishibashi T., Kasahara M.;
A Yoshida M.C., Kirchhoff C., Ishibashi T., Kasahara M.;
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A Yoshida M. Yoshida M.;
A Yoshida M. Yoshida M.;
A Yoshida M.
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P54107; 013248; 000698; 014082;
01-0CT-1996 (Rel. 34, Created)
15-JUN-2002 (Rel. 34, Last sequence update)
Cysteine-rich secretory protein-l precursor (Acidic epididymal glycoprotein homolog) (AEG-like protein) (ARP).
AEGLI OR CRISP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hokkaido
[3]
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MEDLINE-96435914; Pubmed-8838800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Analygis of the human acidic epididymal glycoprotein-like molecule:
isolation of cDNA and tissue localization.";
Hokkaido Igaku Zasshi 70:743-753(1995).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Best Local S
Matches 51
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EMBL; S95238; CAA64525.1;
EMBL; S95238; CAA635899.1;
EMBL; D36451; BAA07483.1;
Genew; HGNC:304; AEGL1.
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P35794;
01-JUN-1994 (R
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01-JUN-1994 (R
FITITING body)
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VARSPLIC
VARSPLIC
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CONFLICT
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SMART; SMO0198; SCP_AG5_PR1_SC7_1; 1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
                                                                                                                                                                                                                                                                                                                              Fruiting body protein SC7 precursor.
SC7:
SChizophyllum commune (Bracket fungus).
Schizophyllum commune (Bracket fungus).
Sukaryota: Fungi; Basidiomycota: Bymenomycetes; Homobasidiomycetes;
Agaricales; Schizophyllaceae; Schizophyllum.
NCBI_TaxID-5334;
                                         -I- SUBCELLULAR LOCATION: Secreted.
-I- DEVELOPMENTAL STAGE: EXPRESSED ONLY IN FRUITING DIKARYONS.
-I- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
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ProDom; PD000542; Allrgn_V5/Tpx1;
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een the Swiss Institute of Bio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -KNGK------TSNIANMYWDSHDKLGCAVVDC----SGKTHVVCQY-----GPEAK.144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QFNKLVTDLPNVQEEIVNIHNALRRRVVP--PASNMLKMSW------SEEA
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0188; SCP; 1.
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230
178
179
22
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97
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(Rel. 29, Last sequence up
(Rel. 29, Last annotation
dy protein SC7 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.5%;
ilarity 23.7%;
Conservative
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                                                                                                                                           139:2083-2090(1993).
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178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYSTEINE-RICH SECRETORY PROTEIN-1.

N-LINKED (GLCNAC. . .).
E -> D (IN SHORT ISOFORM).
E -> D (IN SHORT ISOFORM).
K -> E (IN REF. 2 AND 3).
T -> A (IN REF. 2 AND 3).
M7 -> A (IN REF. 2 AND 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 94.5; D
Pred. No. 0.19
22; Mismatches
                                                                                                                                                                                                                                                  S.A.,
  yht. It is produced Bioinformatics and
                                                                                                                                                                                                                                                                                                                                                                                                                                                         on update)
                                                                                                                                                                                                                                                Kothe E.M.,
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    and
                                                                                                                                                                                                                                                Scheer J.M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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  through a d the EMBL
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collaboration - L outstation -
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AEG_RAT

ID AEG
AC P12

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Best Local S
Matches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01202);
01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence updated)
15-JUN-2002 (Rel. 41, Last annotation updated)
15-JUN-2002 (Rel. 41, Last annotation updated)
15-JUN-2002 (Rel. 10, Last annotation updated)
15-JUN-2002 (Rel. 10)
15-JUN-2002 (Rel. 10)
16-JUN-2002 (Rel. 10)
17-JUN-2002 (Rel. 10)
18-JUN-2002 (Rel. 12)
18-JUN-2002 (Rel.
                                                                                                                                                                                                                    SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

TISSUE-Epididymis;

MEDILINE-8705395; Pubmed-3780731;

BIOONS D.E., Means A.R., Wright E.J., Singh S.P., Tiver K.K.;

MCDLEULar cloning of the CDNA for androgen dependent sperm-coating glycoproteins secreted by the rat epididymis.";

T. Biochem. 161:13-18(1985).
SEQUENCE FROM N.A.

MEDLINE-89039913; PubMed-2460753;

MEDLINE-89039913; PubMed-2460753;

Charset N.J. Joseph D.R., Wilson E.M., French F.S.;

Charlest N.J. Joseph D.R., Wilson E.M., French F.S.;

Molecular cloning of complementary deoxyribonucleic acid
androgen-regulated epididymal protein: sequence homology
metalloproteins.";

Mol. Endocrinol. 2:999-1004(1988).

1- FÜNCTION: THIS PROTEIN IS SUPPOSED TO HELP SPERMATOZO

--- FÜNCTIONAL MATURATION WHILE THEY MOVE FROM THE TESTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
CARBOHYD
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probom; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM0198; SCP; 1.
PROSITE; PS010109; SCP_AG5_PR1_SC7_1; 1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
FRUITING body; Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AEG_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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InterPro; IPR
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PF00188; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity 21.6
35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AADWASQCIWEHSNSGQNLAAWFSPQANKPMNISQGVGGWNAEEPDYNTTTYSGAGHWTQ
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134
204 AA;
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80 N
118 N
134 N
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Pred. No. 0.17
23; Mismatches
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N-LINKED (GLCNAC...) (POUR PROTEIN SC7)

N-LINKED (GLCNAC...) (POUR PROTEIN SC7)

N-LINKED (GLCNAC...) (POUR PROTEIN SC7)

47F1CB45ADFAZFC9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENT I AL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                on update)
c (SCP) (Acidic
) (Protein IV)
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   SPERMATOZOA
THE TESTIS
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(Sialoprotein)
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(POTENTIAL).
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Murinae; Rat
                                                                                                                                                                 acid
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   NA UNDERGO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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RESULT 35
PR12-BORVU
ID PR12-2
AC P3579
DT 01-VI
DT 15-VI
DT 15-VI
DE Patte
OC Bukas
OC Eukas
OC Trit.
OX NCBL
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Best Local S
Matches 45
                        RIZ_HORVU STANDARD; PRT; 164 AA.

D PRIZ_HORVU STANDARD; PRT; 164 AA.

C P35792;

T 01-JUN-1994 (Rel. 29, Created)

T 01-JUN-1994 (Rel. 29, Last sequence update)

T 15-JUN-2002 (Rel. 41, Last annotation update)

Pathogenesis related protein PRB1-2 precursor.

S Hordeum vulgare (Barley).

C Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra

C Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poacea

C Triticaea; Hordeum.

X NCBL_TaxID-4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1
Sperm; G1ycoprotein; Signal.

SIGNAL
1 19
SPERM-COA:
MOD_RES 20 246
CARBOHYD 32 32 N-LINKED
CARBOHYD 147 147
CARBOHYD 213 N-LINKED
CARBOHYD 214 N-LINKED
CARBOHYD 215 N-LINKED
CARBOHYD 215 N-LINKED
CARBOHYD 216 N-LINKED
CARBOHYD 217 N-LINKED
CARBOHYD 218 N-LINKED
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Pfam; PP00188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
Probom; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X04643; CAA28304.1; -.
EMBL; M31173; AAB59716.1; -.
PIR; A4609; A24609
PIR; A40918; A40918.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOCTUS DEFERENS.
INDUCTION: By Androgens.
INDUCTION: By Androgens.
MISCELLANGOUS: SCP IS AN ANDROGEN-DEPENDENT PROTEIN, WHICH IS SECRETED BY THE EPIDIDYMAL EPITHELIUM AND THEN BECOMES ASSOCIATED WITH THE SPERM SURFACE. TWO MAJOR VARIANT PROTEIN D AND E DIFFER FROM EACH OTHER BY THEIR CARBOHYDRATE SIDE CHAINS.
SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1; INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SRCSDYGAGVTCDD 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGENLFMA----NYPASWSSVIQDWYDESLDFVFGFGPKKVGVKVGHYTQVVWNSTFLVAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNCGDLKKMVSCDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVAECPDQPLKYFYVCHYCPGGNYVGRLYSPYTEGEPCDSCPGNCEDGLCTNSCEYEDNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AVVDCSG---KTHVVCQYGPEAKGDGK--TIYEEGAPC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---DVFSAATLNIPLEAGN---SWWSEIFE-LRGKVYNKNG-KTSNIANMVWDSHDKLGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VQEETINKHNQLRRTVSPS--GSDLLRVEWDHDAYVNAQKWANRCIYNHSPLQHRTTTLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MREMFTELHNGYRAAFARNYKTSKMRTMVYDCTLEEKAYKSAEKCSEEPSSEEENV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.4%; Score 94; DB 1; Length 246;
23.2%; Pred. No. 0.21;
Live 23; Mismatches 82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPERM-COATING GLYCOPROTEIN:
BLOCKED (POTENTIAL):
N-LINKED (GLCNAC...) (POTENTIAL):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>. . .</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 82
                                                                                                           ta; Tracheophyta;
Poaceae; Pooideae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214
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RESULT 36
PR13_HORVU
ID PR13_HORVU
ID PR13_94
AC 935793;
DT 01_JUN-1994
DT 15_JUN-2002
DE PAThogenesis
OS HORDENTO VILES
OC EUKATYOTA;
VC SPETMATCOPHYT
OC TITICEAE; H
OX NCBL_TAXID=4;
RN [1]
RP SEQUENCE FROM
RC STRAIN=CV. FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STITTING BRARARARA COCCOCCCCC CCRRARA CO
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Best Local S
Matches 36
                                                           01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pathogenesis-related protein PRBI-3 precursor (PR-IB) (HY-8).
Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Pooldeae;
Triticeae; Hordeum.
NCBI_TaxID-4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant defense;
SIGNAL
CHAIN
MOD_RES 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Gene family encoding basic pathogenesis-related 1 proteins in barley.";
plant Mol. 16:503-507(1994).

1- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS AGAINST PATHOCENS.

1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00188; SCP; 1
PRINTS; PR00837; V5TPXLIKE
PT0Dom; PR000542; Alizgn_V5/TpX1; 1
SMART; SM00198; SCP; 1
PR0SITE; PS01009; SCP_AG5_PR1_SC7_1;
PROSITE; PS01010; SCP_AG5_PR1_SC7_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; 226320; CAA81229.1; -. PIR; S37188; S37188. HSSP; P04284; 1CFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-CV. PSAKNON RESISTANT; TISSUE-Leaf;
MEDLINE-95036024; PubMed-7524728;
MOURADOV A., MOURADOVA E., SCOTT K.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro
EQUENCE FROM N.A. TRAIN-CV. PSAKNON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80
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5
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36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAVVDCSGK--THVVCQYGPEAKGDGKTIY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIFWGSAGADWKAADAVNSWVNE----KKDYNYGSNTCAAGKVCGHYTQVVWRASTSIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NVDVFSAATLNIPLEAGNSWWSEIFELRGKVYNKNGKT-----SNIANMVWDSHDKLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HNAARSAVGVGAVSWSTKLQAFAQNYANQR----INDCKLQHSG------GPYGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HNGYRA-----AFARNYKTSKMRTMVYDCTLEEKAYKSAEKCSEEPSSEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARVVCNNNRGVFITCNYEPRGNIVGQKPY 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR001283; Allrgn_V5/Tpx1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68
113
135
164 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109; SCP_AG5_PR1_SC7_1; 1.
10; SCP_AG5_PR1_SC7_2; 1.
10; SCP_AG5_PR1_SC7_2; 1.
10; SCP_AG5_PR1_SC7_2; 1.
10; SCP_AG5_PR1_SC7_2; 1.
11; Strain-strain in the strain in the 
   resistant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17679 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 92.5;
Pred. No. 0.
      and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDB722DB74EFE390 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
      ÇV.
      NK1558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79
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RESULT 37
VA5_VESMA
ID VA5_V
AC P8165
DT 15-JU
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Best Local S
Matches 37
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DISULFID
DISULFID
SEQUENCE
                       15-JUL-1999 (Rel. 38, Created)
                                                                            VA5_VESMA
P81657;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PODOM; PDUUUUW,
MART; SN00198; SCP; 1.
MART; SN00198; SCP, AG5_PR1_SC7_1; 1.
PROSITE; PS01009; SCP_AG5_PR1_SC7_2; 1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_1; 1.
PROSITE; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S37189; S37189.
PIR; S37209; S37209.
PIR; S37167; S37167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z26321; CAA81230.1; -.
EMBL; Z26333; CAA81234.1; -.
EMBL; X74940; CAA52894.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGAINST PATHOGENS.

-1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00188; SCP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        **Purification, characterization, and molecular cloning of basic PR-1-type pathogenesis-related proteins from barley.*;
Mol. Plant Microbe Interact. 7:267-275(1994).

-1- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bryngelsson T., Sommer-Knudsen J., Gregersen P.L., Collinge D.B.,
EK B., Thordal-Christensen H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-cv. Pallas; TISSUE-Leaf;
MEDLINE-94281675; PubMed-8012045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plant Mol. Biol. 26:503-507(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-95036024; PubMed-7524728;
Mouradov A., Mouradova E., Scott K.J.;
"Gene family encoding basic pathogenesis-related 1 proteins in
barlay ".
                                                                                                                                                                                                                                                                                                                                                                                       124 CAVVDCSGK--THVVCQYGPEAKGDGKTIY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 HNGYRA-----AFARNYKTSKMRTMVYDCTLEEKAYKSAEKCSEEPSSEEE 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P04284;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NVDVFSAATLNIPLEAGNSWWSEIFELRGKVYNKNGKT-----SNIANMVWDSHDKLG 123
                                                                                                                                                                                                                                                                                                           CARVVCNNNRGVFITCNYEPRGNIVGQKPY 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HNAARAAVGVGAVSWSTKLQAFAQNYANQR----INDCKLQHSG-------GPYGE 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIFWGSAGADWKASDAVNSWVSE-----KKDYDYGSNTCAAGKVCGHYTQVVWRASTSIG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR001283; Allrgn_V5/Tpx1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68
113
                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 B
119 B
150 B
17697 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 92.5; DB 1;
Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PATHOGENESIS-RELATED PROTEIN PRB1-3.
PYRROLIDONE CARBOXYLIC ACID
(BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DA4B279B9F5C50C6 CRC64;
                                                                                                             202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 38
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Best Local
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         STRAIN-cv. Samsun NN;
MEDLINE-88083595; PubMed-3691804;
Ohshima M., Matsuoka M., Yamamoto
                                                                                                                                                                      Nucleic [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "PRIA_TOBAC STANDARD; PRT; 168 AA.
1908299; (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
101-AUG-1988 (Rel. 08, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
18-AURO-1992 (Rel. 41, Last annotation update)
18-AURO-1992 (Rel. 41, Last annotation update)
18-AURO-1992 (Rel. 41, Last annotation update)
18-AURO-1993 (PR-1A).
18-AURO-199
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                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-cv. Samsun NN;
MEDLINE-88015528; PubMed-3658669;
                                                                                                                                                                                                                                                  "Structure of tobacco genes encoding pathogenesis-related proteins from the PR-1 group.";
                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                         Cornelissen B.J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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15-JUL-1999 (Rel. 38, Last annotation update)
Venom allergen 5 (Antigen 5) (AG5) (Allergen Vesp m 5).
Vespa mandarinia (Hornet).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS01009; SCP_AG5_PR1_SC7_1; PROSITE; PS01010; SCP_AG5_PR1_SC7_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea;
Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; F
Aculeata; Vespoidea; Vespidae; Vespinae; Vespa.
NCBI_TaxID-7446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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ubmitted (FEB-1998) to the SWISS-PROT data bank.
ubmitted (FEB-1998) to the SWISS-PROT data bank.
usmitarity: BELONGS TO A FAMILY THAT GROUPS MAM
INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1
interPro; IPRO01283; Allrgn_V5/Tpx1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 HYTOMVWAKTKEIGCGSIKYIENGWHRHYLVCNYGPAGNIGNEPIYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 NIANMYWDSHDKLGCAVVDC--SG--KTHVVCQYGPEAKGDGKTIYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 CDYGHDVCRNTAKYSVGQNIAENGSTAASFASVSNMVQMWADEVKNYQYGSTKNKLIEVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 C-----SEEPSSEEENV--DVFSAATLNIPLEAGNSWWSEIFELR-GKVYNKNGKTS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40 EKLE----ILKQHNEFRQKVARGLETRGKPGPQPPAKSMNTLVWNDELAQIAQVWAGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00188; SCP;
                                                                                                                                                                                                  e PR-1 group.";
Acids Res. 15:6799-6811(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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101 B
94 B
185 B
22547 MW;
                                                                                                                                                                                                                                                                                                                                                               Horowitz J., van Kan J.A.L., Goldberg R.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.3%; Score 92.5; DB 1; Length 202; 23.4%; Pred. No. 0.23;
Yamamoto N., Tanaka Y., Kano-Murakami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27;
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STRAINE-OV. Xanthi;
MEDLINE-99041576; PubMed-3186451;
Cutt J.R., Dixon D.D., Carr J.P., Klessig D.F.;
"Isolation and nucleotide sequence of cDNA clones
pathogenesis-related proteins PRIA, PRIB and PRIC
tabacum cv. Xanthi nc induced by TMV infection.";
Nucleic Acids Res. 16:9861-9861(1988).
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STRAIN-CV. Wisconsin 38;

Pfitzner U.M., Pfitzner A.J.P., Goodman H.M.;

Phitzner U.M., Pfitzner A.J.P., Goodman H.M.;

**DNA sequence analysis of a PR-la gene from tobacco:

relationship of heat shock and pathogen responses in

Mol. Gen. Genet. 211:290-295(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Dixon D.C., Cutt J.R., Klessig D.F.;
"Differential targeting of the tobacco PR-1 pathogenesis-related proteins to the extracellular space and vacuoles of crystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ozeki Y., Kato A., Harada N., Ohashi Y.; "Nucleotide sequence of the PR-1 gene of Nicotiana tabacum."; FEBS Lett. 225:243-246(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unfamiliar proteins.";
EMBO J. 4:2745-2749(1985).
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*Amino acid sequence
from viroid-infected
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O J. 10:1317-1324(1991).

FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF FAGAINST PARTHOGENS.

SUBCELLULAR LOCATION: ACCUMULATE IN WITHIN THE VACUOLES SPECIALIZED CELLS KNOWN AS CRYSTAL IDIOBLASTS.

INDUCTION: SYNTHESIZED DURING PATHOGEN INFECTION OR OTHE RELATED RESPONSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTM: THREE DISULFIDE BONDS ARE PRESENT (BY SIMILARITY).
SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMALIAN SCP/TPX1;
INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
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Camacho
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z A., Lottspeich F.,
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       PATHOGENESIS-RELATED
LF -> VS (IN REF. 4).
D -> S (IN REF. 5).
SQ -> PS (IN REF. 5).
                                                                                                            protein;
d REF.
5).
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                                                                                                              Multigene
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Nicotiana
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                                                                                                              family;
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Best Local S
Matches 37
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PIR; S32002; S32002.

PIR; S32474; S39474

HSSP; P04284; ICFE
InterPro; IPR001283; Allrgn_V5/Tpx1.

Pfam; PF00188; SCP; 1.

PRINTS; PR000837; V5TPXLIKE.

PRODOm; P0000842; Allrgn_V5/Tpx1; 1.

PMART; SM00198; SCP; 1.

PROGETTE: B000198; SCP; 1.
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01-JUN-1994 (Rel. 29, Last sequer
15-JUN-2002 (Rel. 41, Last annote
Pathogenesis-related protein 1 pr
Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Strepte
Spermatophyta; Magnoliophyta; Lil
Triticeae; Hordeum.
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Q05968;
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MEDLINE-9403324; PubMed-8219079;

MURADOV A., Petrasovits L., Davidson A.,

"A CDNA clone for a pathogenesis-related

"A CDNA clone For 
                                                                                                                                                                                                              Plant o
SIGNAL
CHAIN
                                                                                                                                                              MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
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PRO1009; SCP_AG5_PR1_SC7_1; 1.

PRO1010; SCP_AG5_PR1_SC7_2; 1.
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yta; Liliopsida; Poales; Poaceae; Pooideae;
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5 -> T (IN REF. 3).
7 -> W (IN REF. 5).
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C TISUE-Venom;

X MEDIINE-9320363; PubMed-8454859;

X MEDIINE-9320363; PubMed-8454859;

X Sequence analysis and antigenic cross-reactivity of a venom allergen, antigen 5, from horners, wasps, and yellow jackets.";

X J. Immunol. 150:2823-2830(1993).

C 1. SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

CC INSECTS A03/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.

DR PIR; A37329; A37329.

DR HSSP; P04284; ICFE.

DR HSSP; P04284; ICFE.

DR PIRSP; P04284; ICFE.

DR PIRSP; P04284; SCP; 1.

PRANTS; PR001283; Allrgn_V5/Tpx1.

DR PIRSP; P04393; V5TPXLIKE.

DR PRINTS; PR00837; V5TPXLIKE.

DR PRINTS; PR00837; V5TPXLIKE.
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P35759;
O1-JUN-1994 (Rel. 29, Created)
O1-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Venom allergen 5 (Antigen 5) (AG5) (Allergen Pol e 5) (Pol e V).
Pollstes exclamans (Eaper wasp).
Eukaryota; Metazoa, Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Ptarygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
Aculeata; Vespoidea; Vespidae; Polistinae; Polistes.
                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS01009; SCP_AG5_PR1_SC7_1; PROSITE; PS01010; SCP_AG5_PR1_SC7_2; Penom; Allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
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                                                                                                                                                                                                                               Similarity
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LIKLWENEV----KDFNYNTGITKQNFAKIGHYTQMVWGKTKEIGCGSLKYIENKMQNH
                                                                   PAASDMNDLVWNDELAHIAQVWASQCQFLVHDKCRNTAKYPVGQ-NIAYAGGSKLPDVVS 129
                                                                                                     ----SKMRTMVYDCTLEEKAYKSAEKCSEEPSSEEENVDVFSAATLNIPLEAGNS-----
                                                                                                                                        GIHTVCQYGESTKPSKNCAGKVIKSVGPTEEEKKLIVSEHNRFRQKVAQGLETRGNPGPQ
                                                                                                                                                                      GDYSLCQQREKL------DDDMREMFTELHNGYRAAFARNYKT-----
                                  ----WWSEIFELRGKVYNKN------GKTSNIANMVWDSHDKLGCA---VVDCSGKTH
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W; DBE93D07316773B3 CRC64;
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Pred. No. 0.88;
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Pred. No. 0.33;
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                                                                                                                                                                                                                                           Length 205
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HSSP; P04284; 1CFE.
InterPro; IRB001283; Allrgn_V5/Tpx1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V) (Fragment).
Polistes annularis (Paper wasp).
Eukaryota; Metazoa; Arthropoda;
Eukaryota; Meoptera; En
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VA5_POLAN STANDARD; PRT; 209 AA. Q05109; Q05109; Q1FEB-1994 (Rel. 28, Created) Q1-FEB-1994 (Rel. 28, Last sequence update) Q1-NOV-1997 (Rel. 35, Last annotation update) Q1-NOV-1997 (Rel. 35, Last annotation update) Venom allergen 5 precursor (Antigen 5) (AG5) (Allergen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBI outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence analysis and antigenic cross-reactivity of a venom allergen, antigen 5, from hornets, wasps, and yellow jackets."
J. Immunol. 150:283-2830(1993).
-I- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALTAN COD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   zukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea; Vespidae; Polistinae; Polistes.
NCBI_TaxID=27505;
                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS01009; SCP_AG5_PR1_SC7_1; PROSITE; PS01010; SCP_AG5_PR1_SC7_2; Venom; Allergen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD00054
SMART; SM00198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00188; SCP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-93203603; PubMed-8454859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1; INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                134 LIKLWENEV----
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                                                                                                                                                                                                                                           Similarity
                                                                                 PAASDMNDLVWNDELAHIAQVWASQCQFLVHDKCRNTAKYPVGQ-NIAYAGGSNLPDVVS
                                                                                                                                                                                    GDYSLCQQREKL-------DDDMREMFTELHNGYRAAFARNYKT-----
                                            ----WWSEIFELRGKVYNKN------GKTSNIANMVWDSHDKLGCA---VVDCSGKTH 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PD000542;
                                                                                                                 ---SKMRTMVYDCTLEEKAYKSAEKCSEEPSSEEENVDVFSAATLNIPLEAGNS----
                                                                                                                                                  GIHTVCQYGESTKPSKNCAGKVIKSVGPTEEEKKLIVSEHNRFRQKVAQGLETRGNPGPQ
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                                                                                                                                                                                                                                                                                                          209
108
100
192
                                                                                                                                                                                                                                       19.2%;
                                                                                                                                                                                                                                                                                            23293 MW;
              -KDFNYNTGITKONFAKIGHYTONVWGKTKEIGCGSLKYMENNMONH
                                                                                                                                                                                                                       32; Mismatches
                                                                                                                                                                                                                                                                                        BY SIMILARITY.
VENOM ALLERGEN 5.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151
                                                                                                                                                                                                                                         Score 86;
Pred. No.
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                                                                                                                                                                                                                       74;
                                                                                                                                                                                                                                                       Length 209;
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RESULT . VA5_POLI ID VA.A. POLI V

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Query Match Best Local S Matches 38

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133 89 DISULFID DISULFID DISULFID SEQUENCE

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189 YLICNYGPAGNYLGQLPY 206 135 - VVCQYGPEAKGDGKTIY

151

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RESULT 42

RESULT 42

ITBS_HMAN

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                                                                                    EMBL; X53002; CAA37188.1; -.
EMBL; M35011, AAA52707.1; -.
EMBL; J05653; AAA59183.1; -.
EMBL; BC006541; AAH06541.1; -.
PIR; A35775, A35775.
PIR; A35775, A35775.
PIR; $12534; $12534.
PIR; $18308; A38308.
PIR; $13506; A1708.
HSSP; P05106; LTV2.
Genew; HSN2:6505; TTGB5.
MIM; 147561; --
MIM
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE R.

STEAMSDETS R.

SUBMITTED (APR-2001) to the EMBL/GenBank/DDBJ databases.

SUBMITTED R.

SUBMITTES THE SEQUENCE R.G.D IT ITS LIGAND.

IT RECOGNIZES THE SEQUENCE R.G.D IT ITS LIGAND.

SUBMIT: HETERODIMER OF AN ALPHA AND A BETA SUBMIT. BETA-5

ASSOCIATES WITH ALPHA-V.

ASSOCIATES WITH ALPHA-V.

SUBMILLARITY: BELONGS TO THE INTEGERIN BETA CHAIN FAMILY.

SIMILARITY: CONTAINS 1 WHFA-LIKE DOMAIN.

SIMILARITY: CONTAINS 1 WHFA-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Integrin beta-5 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE=90319111; PubMed=2371275;

SUZUKI S., Huang Z.S., Tanihara H.;

"Cloning of an integrin beta subunit exhibiting high homology with integrin beta 3 subunit.";

Proc. Natl. Acad. Sci. U.S.A. 87:5354-5358(1990).

[3]
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TISSUE-Thymic epithelium;
MEDLINE-9028356; PubMed-2328726;
MEDLINE-90228356; PubMed-2328726;
Ramaswamy H., Hemler M.E.;
Rinaswamy H., Hemler M.E.;
Mcloning, primary structure and properties of a novel human integrin beta subunit.";
beta subunit.";
beta Subunit.";
beta Subunit.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE-91009141; PubMed-2211615;

MCLean J.W., Vestal D.J., Cheresh D.A., Bodary S.C.;

MCLean J.W., Vestal D.J., Cheresh D.A., Bodary S.C.;

"CDNA sequence of the human integrin beta 5 subunit.";

J. Biol. Chem. 265:17126-17131(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CBI_TaxID-9606;
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     IPR000561; EGF-like.
IPR002369; Integrin_B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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PRINTS; PR01186; INTEGRINB.
ProDom: PD001811; Integrin_B; 1.
SMART; SM00181; EGF_1:
SMART; SM00001; EGF_1:
SMART; SM00001; EGF_1:
SMART; SM000187; INTEGRIN BETA:
SMART; SM00423; PSI; 1.
SMART; SM00423; PSI; 1.
SMART; SM00327; VWA; 1.
                                                                                                                                       DISULFID
DIS
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PROSITE; PS00022; EGF_1; UNKNOWN_2.
PROSITE; PS01186; EGF_2; UNKNOWN_2.
Integrin; Cell adhesion; Receptor; Transmembrane;
Repeat; Signal.
23 POTENTIAL.
23 POTENTIAL.
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InterPro; IPR003659; Plexin-like.
InterPro; IPR002055; VWF_A.
Pfam; PF00362; Integrin_B; 1.
11 EKLDDDMREMFTELHNGYRAAFARNYKTSKMRTMVYD------CTLEE-KAYKSAE
                                            Similarity 22.0
                                                                                                                                             Ą,
                                                                                                                                             88053 MW;
                                                                      8.6%;
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INTEGRIN BETA-5.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
VWFA-LIKE
4 CYSTEINE-RICH TANDEM REPEATS.
                                                                                                                                          III.

III.

IV

BY SIMILARITY
BY GILCUAC.
N-LINKED (GLCNAC.
N-LINKED (
                                                     31;
                                                     Score 86; DB Pred. No. 4.6; Mismatches
                                                                                                    1;
                                                        66;
                                                                                                 Length 799
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                                                        Indels
                                                           84;
                                                           Gaps
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RESULT 43
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MEDLINE-20033487; PubMed-10617197;

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,

Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,

Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,

Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,

Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN=cv. Landsberg erects; TISSUE-Leaf;
MEDLINE-9005717; PubMed-139289;
MEDLINE-9005717; PubMed-139289;
MILLINE-9005717; PubMed-139289;
Oknes S., Mauch-Mani B., Moyer M., Potter S., Will
Dincher S., Chandler D., Slusarenko A., Ward E.,
"Acquired resistance in Arabidopsis.";
"Acquired resistance in Arabidopsis.";
"Plant Cell 4:645-656(1992).
                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
              EMBL; M90508; AAA32863.1; -. EMBL; AC005398; AAC69381.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                    "Sequence and analysis of chromosome 2 of the plant Arabidopsis thallana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PR1_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=3702
                                                                                                                                                                                                                            INDUCTION: INDUCED BY 2.6-DICHLOROISONICOTINIC ACID (INA) AND SALICYLIC ACID (POSSIBLY AN ENDOGENOUS SIGNAL FOR ACQUIRED RESISTANCE). STRONGLY INDUCED BY PATHOGEN INFECTION. SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1; INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: ACCUMULATES IN THE APOPLAST BEFORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 MVWDSHDKLGCAV-----VDCSGK-THV--VCQYGPE-----AKGDGKTIYE---- 152
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JQ1693
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protein 1 precursor (PR-1).
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ID PO9042

PRIC_TOBAC

ID PO1-APR

PO 11-5-UN

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RP SEQUEN

RA CUET

RA FILSOLA

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PRINTS; PRO0037; Allrgn_V5/Tpx1; 1.

SMART; SM00198; SCP; 11.

PROSITE; PS011009; SCP_AG5_PR1_SC7_1; 1.

PROSITE; PS011010; SCP_AG5_PR1_SC7_2; 1.

Plant defense; Signal; Pathogenesis-related protein.
                                                                                                                                                                                                                          STRAIN-ov. Xanthi;

MEDLINE-89041576; PubMed=3186451;

Cutt J.R., Dixon D.D., Carr J.P., Klessig D.F.;

Cutt J.R., Dixon D.D., Carr J.P., Klessig D.F.;

"Isolation and nucleotide sequence of cDNA clones for the pathogenesis-related proteins PRIA, PRIb and PRIc of Nicotiana tabacum cv. Xanthi nc induced by TMV infection.";

Nucleic Acids Res. 16:9861-9861(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1988 (Rel. 09, Created)
01-NPR-1990 (Rel. 14, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pathogenesis related protein 1C precursor (PR-1C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P09042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P04284; 1CFE. InterPro; IPR001283; Allrgn_V5/Tpx1
STRAIN-cv. Samsun NN;
MEDLINE-87231077; PubMed-3295779;
Pfitzner U.M., Goodman H.M.;
"Isolation and characterization of cDNA clones encoding pathogenesis-
related proteins from tobacco mosaic virus infected tobacco plants.";
Nucleic Acids Res. 15:4449-4465(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nicotlana tabacum (Common tobacco).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledona; core eudicota;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotlana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-cv. Samsun NN; TISSUE-Leaf;
MEDLINE-90174915; PubMed-2308825;
Ohshima M., Harada N., Matsuoka M., Ohashi Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOD_RES
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                                                                                                                                                                        SEQUENCE OF 8-168 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 6-168 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic Acids Res. 18:182-182(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The nucleotide sequence of pathogenesis-related (PR) 1c protein gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOBAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 VVWRKSVRLGCAKVRCNNGGTIISCNYDP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 MVWDSHDKLGCAVVDC-SGKTHVVCQYGP 141
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113
133
161 AA;
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161
27
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117
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23.5%; Pred. No. 0.
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protein

gene

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RESULT 45
PRIB_TOBAC
ID PRIB_T
AC PO7053
DT 01-APR
DT 01-APR
DT 15-JUN
DE PRIBOT
OC ENARY
OC ENARY
OC ASTETM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 38; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S07580; S07580.

HSSP; P04284; LCFE.
InterPro; IFR001283; Allrgn_V5/Tpx1.
Pfam; PF00188; SCP; 1.
PRINTS; PR00837; V5/TpX1KE.
PRODOM; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
    PRIB_TOBAC STANDARD; PRT; 168 AA.
P07053;
01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Pathogenesis-related protein 1B precursor (PR-1B).
Nicotiana tabacum (Common tobacco).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledons; core endicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMARY; SMOID8; SCP; 1.
SMARY; SMOID8; SCP, AG5_PR1_SC7_1; 1.
PROSITE; PS01009; SCP_AG5_PR1_SC7_2; 1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
PATHOGENESIS-RELATED PROTEIN 1C.
SIGNAL 1 30
PATHOGENESIS-RELATED PROTEIN 1C.
CHAIN 31 168
PATHOGENESIS-RELATED PROTEIN 1C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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SUBCELLULAR LOCATION.
SUBCELLULAR LOCATION.
MEDLINE-91224081; PubMed-2026137;
Dixon D.C., Cutt J.R., Klessig D.F.;
"Differential targeting of the tobacco PR-1 pathogenesis-related proteins to the extracellular space and vacuoles of crystal idioblasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X17681; CAA35666.1; -.
EMBL; X05454; CAA29023.1; -.
EMBL; X12487; CAA31010.1; -.
                                                                                                                                                                                                                                                                                                                                                 105 NGKT-----SNIANMVWDSHDKLGCAVVDCSGKTHVV-CQYGPEAKGDGKTIY 151
                                                                                                                                                                                                                                                                                                                      114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 CQQREKLDDDMREMFTELHNGYR------AAFARNYKTSKMRTMYYDCTL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10:1317-1324(1991)
                                                                                                                                                                                                                                                                                                                 DSNTCAQGQVCGHYTQVVWRNSVRVGCARVQCNNGGYIVSCNYDPPGNVIGKSPY 168
                                                                                                                                                                                                                                                                                                                                                                                                  CHAQNSQQD----YLDAHNTARADVGVEPLTWDDQVAAYAQNYASQ----LAADCNLVH 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.5%; Score 85; DB 1; Length 168
21.7%; Pred. No. 0.85;
Live 22; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                            Query Match
                                                                                                                                                                                                                                                                                      EMBL; D90197; BAA14221.1; -.
EMBL; X23465; CAA27183.1; -.
EMBL; X12486; CAA31099.1; -.
EMBL; X17680; CAA35665.1; -.
PIR; B24620; B24620.
PIR; S07579; S07579.
HSSP; P04284, 10EE
                                         Plant def
SIGNAL
CHAIN
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-cv. Xanthi;
MEDLINE-89041576; PubMed-3186451;
Cutt J.R., Dixon D.D., Carr J.P., Klessig D.F.;
Cutt J.R., Dixon D.D., Carr J.P., Klessig D.F.;
"Isolation and nucleotide sequence of cDNA clones
pathogenesis-related proteins PRIA, PRID and PRIC
tabacum cv. Xanthi nc induced by TMY infection.",
Nucleic Acids Res. 16:9861-9861(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
STRAIN-CY. Samsun NN; TISSUE-Leaf;
MEDLINE-90174914; PubMed-2308824;
Ohshina M., Harada N., Matsuoka M., Ohashi Y.;
"The nucleotide sequence of pathogenesis-related (PR) 1b
of tobacco.";
Nucleic Acids Res. 18:181-181(1990).
                                                                                                                                                                                  InterPro; IPRO01883; Allrgn_V5/Tpx1.
Pfam; PP00188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
PRODOM; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROW entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-triffic timentitutions as long as its content is non way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-91224081; PubMed-2026137;
Dixon D.C., Cutt J.R., Klessig D.F.;

**Differential targeting of the tobacco PR-1 pathogenesis-related proteins to the extracellular space and vacuoles of crystal idioblasts.**

EMBO J. 10:1317-1324(1991)
                                  PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
Plant defense; Pathogenes1s -related protein; Multigene family; SIGNAL 1 30
PATHOGENESIS-RELATED PROTEIN 1B.
CONFLICT 16 16 S -> A (IN REF. 3).
SEQUENCE 168 AA; 18499 MW; 61FCE3B87A7F31F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAINST PATHOGENS.

-I- SUBCELLULAR LOCATION: ACCUMULATE IN WITHIN THE VACUOLES OF SPECIALIZED CELLS KNOWN AS CRYSTAL IDIOBLASTS.
-I- INDUCTION: SYNTHESIZED DURING PATHOGEN INFECTION OR OTHER STRESS-RELATED RESPONSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ЕМВО J. 5:37-40(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-cv. Samsun NN;
Cornelissen B.J.C., Hooft van H
Bol J.F.;
"MoLecular characterization of
"MoLecular proteins la, lb and lc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 16-168 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RELATED RESPONSES.

PTM: THREE DISTLETE BONDS ARE PRESENT (BY SIMILARITY)

SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MANMALIAN

INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hooft van Huijsduijnen R.A.M., van Loon L.C
  8.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and 1c,
    Score 84.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 messenger RNAs for 'pathogenesis-
c, induced by TMV infection of
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MAMMALIAN SCP/TPX1;

for the of Nicotiana

SOFT WAR BRANK BRA

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Length 168;

		cine: 72 secs	120 DKLGCAVVDCSGKTHVV-CQYGPEAKGDGKTIY 151 ::	### Part Local Similarity 22.2%; Pred. No. 0.95; ###################################
				7; 66 92 119
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us-09-937-555a-2.rspt

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is the number of results predicted by chance to have a ster than or equal to the score of the result being printed, rived by analysis of the total score distribution.
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997
1 EGDYSLCQQREKLDDDMREM......DYGAGVTCDDDWQNLLCIGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          July 15, 2003, 08:32:07; Search time 80 Seconds (without alignments) 466.182 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             671580
                         Q962v9 ancylostoma
Q1696 ancylostoma
Q1696 ancylostoma
Q76744 necator ame
Q9xz41 ancylostoma
Q7721 ancylostoma
Q77153 ancylostoma
Q79152 cooperia pu
Q18519 haemonchus
P90958 caenorhabál
Q4513 haemonchus
Q95144 cooperia pu
Q19348 caenorhabál
Q96314 heterodera
                                                                                                                                                       Description
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                                                            B
                                                                                                Query Match
Best Local Simi
Matches 181;
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Q962V9, G1-DEC-2001 (TrEMBLrel. 19, Crea
O1-DEC-2001 (TrEMBLrel. 21, Last
O1-JUN-2002 (TrEMBLrel. 21, Last
Platelet inhibitor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

DelValle A., Harrison L.M., Cappello M.;

"Cloning of the hookworm platelet inhibitor (HPI) from adult norylostoma caninum";

Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF399709; AAKB1732.1;

InterPro, IPR001283; Allrgn_V5/Tpx1.

Probom; PD000542; Allrgn_V5/Tpx1; 1.

NOM_TER

1
                                                                                                                                                                                                                                     Ancylostoma caninum (Dog hookworm).

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Ancylostomatoidea; Ancylostomatidae; Ancylostomatinae;
NCBI_TaxID=29170;
                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                     121 KLGCAVVDCSGKTHVVCQYGPEAKGDGKTIYEEGAPCSRCSDYGAGVTCDDDWQNLLCIG
                           61
                                           61
                                                                        1 EGDYSLCQQREKLDDDMREMFTELHNGYRAAFARNYKTSKMRTMVYDCTLEEKAYKSAEK
                                                                                               h 100.0%; s
Similarity 100.0%; F
81; Conservative 0;
                         CSEEPSSEEENVDVFSAATINIPLEAGNSWWSEIFELRGKYYKKKKTENIANWYWDSHD 120
                                                              EGDY SLCQQREKLDDDMREMFTELHNGYRAAFARNYKTSKMRTMVYDCTLEEKAYKSAEK
                                                                                                                                     181 AA; 20333 MW; FB5CED6FFE567DAA CRC64;

    Created)
    Last sequence update)
    Last annotation update)

                                                                                                                                                                                                                                                                                                                                                                                                      Q9BIQ6
Q9BIQ6
Q9BIQ6
Q9U5N4
Q8TCBB
Q9UB03
                                                                                                Score 997; DB 5;
Pred. No. 3.8e-85;
): Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                             ₿
                                                                                                                  Length 181;
                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      097149 wuchereria
02060 caenorhabdi
033747 caenorhabdi
030747 caenorhabdi
016854 onchocerca
0920u6 rattus norv
044932 brugta mala
018543 caenorhabdi
09313 caenorhabdi
093746 caenorhabdi
018540 caenorhabdi
018540 caenorhabdi
018540 caenorhabdi
018741 dirofilaria
09537 dirofilaria
09537 dirofilaria
                                                                                                                                                                                                                                                                                                                                                                                                  Q9cq35 mus musculu
Q9d2r3 mus musculu
Q2d2r1 caenorhabdi
Q18539 caenorhabdi
Q18538 caenorhabdi
Q9h108 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8tcb8 homo sapien
Q9h336 homo sapien
Q9ub03 wuchereria
O97149 wuchereria
                                                                                                                                                                                                                                             Strongylida;
Ancylostoma.
                                                                                                 0
         180
                                                             60
```

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

sp_archea:*
sp_bacteria:*

SPTREMBL_21:*
1: Sp_archea:*
2: Sp_bacterian:
3: Sp_fungi:*
4: Sp_human:*
5: Sp_invertebr
6: Sp_manmal:*
7: Sp_manmal:*
7: Sp_manmal:*
10: Sp_plant:*
11: Sp_rodent:*
11: Sp_vrus:*
13: Sp_vrus:*
13: Sp_vrus:*

sp_invertebrate:*
sp_mammal:*
sp_mhc:*

sp_organelle:*
sp_phage:*
sp_plant:*
sp_rodent:*
sp_virus:*
sp_virus:*
sp_vertebrate:*
sp_vertebrate:*

sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*

Minimum DB Maximum DB

seq length: 0 seq length: 2000000000

Total number

of hits satisfying chosen parameters:

671580 seqs, 206047115 residues

Title: Perfect score:

Run on: OM protein

.

protein search, using sw model

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Result No.

Score

% Query Match

Length

B

SUMMARIES

997 290 264.5 264.5 262.6 262.6 261.5 216.5 216.5 219.5 209.5 209.5 209.5 199.5 189.5

100.0 29.1 29.1 26.5 26.5 26.3 26.2 27.7 21.7 21.9 20.9 19.1 19.1 18.5 18.5

222155 22215 22215 22215 22215 22215 22215 22215 22215 22215 22215 22215 22215 22215

Q962V9 Q16962 Q16969 O76744 Q9XX41 O777231 O777231 O771231 O771231 O78152 Q98172 Q981Q4 Q19348 Q19348 Q19348 Q19348 Q19348 Q19348 Q19348 Q19348

Pred. No. is the score greater to and is derived by

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RESULT 2
Q16969
AC Q169
D7 Q169
D7 Q169
D7 Q1-1
D7 Q1-
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Best Local S
Matches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           016969 PRELIMINARY; PRT; 274 AA.
016969; 01-NOV-1996 (TIEMBLIFEL 01, Created)
01-NOV-1996 (TIEMBLIFEL 01, Last sequence update)
01-NOV-1996 (TIEMBLIFEL 21, Last annotation update)
01-UN-2002 (TIEMBLIFEL 21, Last annotation update)
Neutrophil inhibitory factor precursor.
                                                                                                                                                                   076744

076744;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-9493581; PubMed-7908286;
MEDLINE-9493581; PubMed-7908286;
MOyle M., Foster D.L., McGrath D.E., Brown S.M., Laroche Y.,
de Meutter J., Stanssens P., Bogowitz C.A., Fried V.A., Ely J.A.,
Soule H.R., Vlasuk G.P.;
That inhibits neutrophil function is a ligand
of the integrin CDIIb/CDIB.";
J. Biol. Chem. 269:10008-10015(1994).
EMBL; L27427; MAA27789.1;
InterProp. 1FR001283; Alirgn_V5/Tpx1.
Propom. 500010842; Alirgn_V5/Tpx1;
ENDER. 5000108.50.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ancylostoma caninum (Dog hookworm).
Bukkaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Ancylostomatoidea; Ancylostomatidae; Ancylostomatinae; Ancylostoma.
NCBI_TaxID=29170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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Necator americanus.
Eukaryota; Metazoa;
Ancylostomatoidea; /
NCBI_TaxID=51031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 AKGDGKTIYEEGAPCSRCSDY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99 GKVYNKNGKTSNIANMVWDSHDKLGCAVVDC-----SGKT-----HVVCQYGPE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95 EKSAYMSARNCSDSSSPPEGYDENKYIFENSN-NISEAALKAMISWAKEAFNLNKTKEGE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NDSIRLOFLAMHNGYRSKLALGHISITEESESDDDDDDFGFLPDFAPRASKMRYLEYDCEA 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 274 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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30680 MW;
                                                      Ancylostomatidae; Bunostominae; Necator
                                                                                                             Nematoda; Chromadorea; Rhabditida; Strongylida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29.1%; Score 290; DB 5; Length 274; 34.3%; Pred: No. 4.4e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23; Mismatches
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NEUTROPHIL INHIBITORY FACTOR.
; 515808713068DC7E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57; Indels 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                              RESULT 4
Q9XZ41
ID Q9XZ
AC Q9XX
D7 Q1.N
D7 Q1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SO TT WE SERVE THE RESERVE TO THE RESERVE 
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Best Local
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                              SEQUENCE FROM N.A.
STRAIN-SHANGHAI;
STRAIN-SHANGHAI;
MEDLINE-20163524; PubMed-10701589;
MEDLINE-20163524; PubMed-10701589;
Shan Q., Zhan B., Xiao S.-H., Feng Z.
Shan Q., Zhan B., Xiao Imolecules fi
"Variation between ASP-1 molecules fi
and the United States.";
and the United States.";
J. parasitol. 8:181-185(2000).
EMBL; AR132291, AAD31839.1;
HSSP; P04284; ICFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIJINE-96315086; PubMed-8636085;
MEDIJINE-96315086; PubMed-8636086;
MEDIJINE-96315086; PubMed-8636086;
MEDIJINE-96315086; PubMed-8636086;
MEDIJINE-96315086; PubMed-8636086;
MEDIJINE-96315086; PubMed-8636086;
MEDIJINE-96315086; PubMed-8636086;
MEDIJINE-96315086; PubMed-8636086; PubMed-
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SEQUENCE FROM N.A.
STRAIN-SHANGHAI;
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pRINTS; PR00837; V5TPXLIKE.
probom: PD000542; Allrgn_V5/Tpx1; 2.
smarT; SM00198; SCP; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OSYZ41 PRELIMINARY; PRT; 424 AA.

GSYZ41;
GSYZ42;
GSZZ42;
GSZZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOI. Blochem. Parasitol. 98:143-149(1999).
EMBL; AP079521; AAD13340.1; -.
HSSP; P04284; ICFE.
InterPro; IPR001283; Allrgn_V5/Tpx1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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Shu-hua X., Tiehua L., Xing G., Zheng F., Hotez P.;
Ancylostoma secreted protein 1 (ASP-1) homologues in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EQUENCE FROM N.A.
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Biol. Chem. 271:6672-6678(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      347 ALWNRPNMQIGHYTQMAWDTTYKLGCAVVFCNDFTFGVCQYGPGGNYMGHVIYTMGQPCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           159 RCSDYGAGVTC 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 SAEKCSEEPSSEEE----NVDVFSAATLNI-----PLEAGNSWWSEIFE-----LRG 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 Similarity 32.5 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 CQQREKLDDDMREMFTELHNGYRAAFARNY------KTSKMRTMYYDCTLEEKAYK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QCS---PGATC 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       424 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 P
424 A
45742 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.5%; Score 264.5; DB 5; Length 424;
32.5%; Pred. No. 1.8e-16;
Live 27; Mismatches 71; Indels 31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
ANCYLOSTOMA SECRETED PROTEIN 1.
, BF1EB2F95F9B4A9F CRC64;
                                                                                                                                                                                                                                                  Z., I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      424 AA.
                                                                                                                                                                                                                                            Hotez P., Hav
n Ancylostoma
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Hawdon J.M.; oma caninum in China

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                                                                                                                                 Mol. Blochem.
Mol. Blochem.
EMBL; AF089728; AAC35700.
EMBL; AF089728; AAC35700.
HSSP; P042184; 1CFE.
R InterPro; IPRO01283; Allrgn_V5/Tpx1.
R Pfam; PF00188; SCP; 1.
R PRINTS; PR00837; V5TPXLIKE.
PRINTS; PD000542; Allrgn_V5/Tpx1; 1.
                                                  Query Match
Best Local S
Matches 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 62
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-BALTIMORE;
MEDLINE-99270306; PubMed-10340481;
Hawdon J.M., Narasimhan S., Hotez P.J.;
Hawdon J.M., Narasimhan S., Hotez P.J.;
"Ancylostoma secreted protein 2: cloning and characterization second member of a family of nematode secreted proteins from Ancylostoma caninum.";
Ancylostoma caninum.";
Mol. Biochem. Parasitol. 99:149-165(1999).
                                                                                                                                                                                                                                                                                                                                                                                   077221;
01-NOV-1998 (TEMBLrel. 08, Creat
01-NOV-1998 (TEMBLrel. 08, Last
01-JUN-2002 (TEMBLrel. 21, Last
Secreted protein ASP-2 precursor.
ASP-2.
                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Ancylostomatoidea; i
NCBI_TaxID=29170;
                                                                                                                                                                                                                                                                                                                                             Ancylostoma caninum (Dog hookworm).

Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Bukaryota; Metazoa; Ancylostomatidae; Ancylostomatinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        077221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam; PF00188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpx1; 2.
SMART; SM00198; SCP; 2.
                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G
                                                                                                                                                                                                                      Biochem. Parasitol. 99:149-165(1999). AF089728; AAC35986.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            347
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      27
                           13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 COOREKLDDDMREMETELHNGYRAAFARNY------KTSKMRTMVYDCTLEEKAYK
                                                          Similarity
                    LDDDMREMFTELHNGYRAAFARNY------KTSKMRTMYYDCTLEEKAYKSAEKCS 62
MTDEARQKFLDVHNSYRSMVAKGQAKDAISGNAPKAAKMKKMIYDCNVESTAMQNAKKCV 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KYYNK-NGKTSNIANMYMDSHDKLGCAVYDCSGKTHYVCQYGPEAKGDGKTIYEEGAPCS 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RCSDYGAGVTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALWNRPNMQIGHYTQMAWDTTYKLGCAVVFCNDFTFGVCQYGPGGNYMGHVIYTMGQPCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HGNKCVYQHSHGEDRPGLGENIYKTSVLKEDKNKAAKQASQLWWNELKEYGVGPSNVLTT
                                                                                             19
19
218 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                424 AA;
                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                     SCP_AG5_PR1_SC7_1; 1.
                                                                                          18 E
218 S
23954 MW;
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45761 MW;
                                                          26.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169
                                                38;
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Last sequence up
Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27;
                                                          Score 262; DB 5;
Pred. No. 1.3e-16;
                                                                                       POTENTIAL.
SECRETED PROTEIN ASP-2.
BC263DEA808AAF6F CRC6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 264.5; DB >;
Pred. No. 1.8e-16;
Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
ANCYLOSTOMA-SECRETED PROTEIN 1.
8409CDF8AECD248E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      218
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lon update)
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                                               69;
                                                                   Length 218;
                                               Indels
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                                                                                                                                                                                                                                                                                                                                                Strongylida;
Ancylostoma.
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                                               26;
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                                           Gaps
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                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 64
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SEQUENCE
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077153;
01-NOV-1998
01-NOV-1998
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpx1;
SMART; SM00198; SCP; 2.
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Ancylostomatoidea; Ancylostomatidae; Ancylostomatinae; Ancylostoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1998 (TIEMBLEEL 08, 01-NOV-1998 (TIEMBLEEL 08, 101-JUN-2002 (TIEMBLEEL 21, 1101-JUN-2002 (TIEMBLEEL 21, 1101-JUN-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bin Z., Hawdon J., Qiang S., Hainan R., Huiqing Q., Wei H.,
Shu-hua X., Tiehua L., Xing G., Zheng F., Hotez P.;
Ancylostoma secreted protein 1 (ASP-1) homologues in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIINE-96215086; PubMed-8636085;
Hawdon J.M., Jones B.F., Hoffman D.R., Hotez P.J.;
*Cloning and characterization of Ancylostoma-secreted protein. A novel protein associated with the transition to parasitism by infective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-SHANGHAI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-SHANGHAI;
MEDLINE-99151774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=51022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nterPro;
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159
                                          348
                                                                                           100
                                                                                                                                         288
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AF077402; AAD13339.1; -.
PFO; IPR001183; Allrgn_V5/Tpx1.
PF00188; SCP; 1.
                                                                                                                                                                                         57
                                                                                                                                                                                                                                                                                                                                     64;
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                                                                                                                                                                                                                                                                                                                               Similarity 33.5
64; Conservative
RCSDYGAGVTC 169
                                                                       KVYNKNG-KTSNIANMVWDSHDKLGCAVVDCSGKTHVVCQYGPEAKGDGKTIYEEGAPCS 158
                                       ALWINRPGMQIGHYTQMAWDTTYKLGCAVVFCNDFTFGVCQYGPGGNYMNHLIYTMGQPCS
                                                                                                                                   HGNKCYYQHSSGNDRPGLGENIYKTSVQKFEKNKAAKQASELWWNELREFGVGPSNNLTN
                                                                                                                                                                                 SAEKCSEEPSSEE-----ENVDVFSAATL---NIPLEAGNSWWSEIFE-----LRG
                                                                                                                                                                                                                              CPSNTGMTDSVRDTFLSLHNGFRSSVARGLEPDALGGNAPKAAKMLKMVYDCEVEASAIR
                                                                                                                                                                                                                                                                   CQQREKLDDDMREMFTELHNGYRAAFARNY-----KTSKMRTMYYDCTLEEKAYK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FAHSHRKGVGENIWMSTAROMDKAQAAQQASDGWFSELAKYGVGQENKLTTQLWNRGVMI
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20
425 AA;
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425 A
45821 MW;
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Last sequence update)
Last annotation updat
n 1 precursor.
                                                                                                                                                                                                                                                                                                                                  Score 261.5;
Pred. No. 3.4e
23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
ANCYLOSTOMA-SECRETED PROTEIN; 1F6B9D7E62EEDDA8 CRC64;
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ies 73;
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                                                                                                                                                                                                                                                                                                                                                                          Length 425;
                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                               31;
                                                                                                                                                                                                                                                                                                                             Gaps
                                     407
                                                                                                                                   347
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RESULT OF BIPS OF BIPS
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AC 0185
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Best Local S
Matches 57
                                                                                                                                                                                                                                                                                   Ol8519 PRELIMINARY; PRT; 222 AA.

018519; O1-JAN-1998 (TIEMBLTel. 05, Created)
01-JAN-1998 (TIEMBLTel. 05, Last sequence update)
01-JUN-2002 (TIEMBLTel. 01, Last annotation update)
01-JUN-2002 (TIEMBLTel. 21, Last annotation update)
24 kDa excretory/secretory protein.
Haemonchus contortus (Barber pole worm).
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Stron
Trichostrongyloidea; Haemonchidae; Haemonchinae; Haemonchus.
NCBL_TaxID-6289;
SEQUENCE FROM N.A.

MEDLINE-97418804; PubMed-9274880;

Schallig H.D., van Leeuwen M.A., Verstrepen B.E., Cornelissen A.W.;

Schallig H.D. van Leeuwen de expression of two putative protectification and expression of two putative protectifications of Haemonchus contortus.";

Mol. Blochem. Parasitol. 88:203-213(1997).
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF352714; ARX55199.1;
HSSP; P04284; ICFE.
HSSP; P04284; ICFE.
HSSP; D04284; ICFE.
InterPro; IPR001283; Allrgn_V5/Tpxl.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
Activation associated secreted protein-like protein (Fragment).
Cooperia punctata.
Cooperia punctata.
Chromadores, Rhabditida; Strongylida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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NCBI_TaxID-96640;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155
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S; PR00837; V5TPXLIKE
m; PD000542; Allrgn_V
; SM00198; SCP; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75
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57; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AYKSAE-KCSEEPSSEEE------NVDVFSAATLNIPLEAGNSWWSEIFELRG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPCMKNEDCKC-TNCTCSKGEALCI 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APCSRCSDYGAGVTCDDDWQNLLCI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVPPDNKYTRNIDAYDYSQMVWQNSYKIGCVVASCSSMTWVACGYSPAGNIDGSLIYELG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----KYYNKNGKTSNIANNYWDSHDKLGCAVVDCSGKTHVVCQYGPEAKGDGKTIYEEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MMKWAQAQCAYAPFKSDKHYGRNTWGMGIPNYNKTAAAESSV-----DDWFD---ELRSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALCSLNNGMTDEVRKLFLDKHNEYRSLVAKGQAPNPVFGGNTSKAARMLKVRYDCEVEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLCQQREKLDDDMREMFTELHNGYRAAFARNY-----KTSKMRTMVYDCTLEEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               465 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.7%;
ilarity 27.8%;
Conservative ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Allrgn_V5/Tpx1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51628 MW;
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Pred. No. 5.9e-12;
0; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                    Strongylida;
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                                                                                       protective
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Best Local S
Matches 59
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Best Local S
Matches 58
                                                                                                                                                                                                                                                    EMBL; 268108; CAA92136.1; ...
HSSP; P04284; 1CFE.
InterPro; IPR01283; Allrgn_V5/Tpxl.
Pfam; PF00188; SCP; 1.
PRINTS; PR000837; V5/TpxlIKE.
PRODOM; PD000542; Allrgn_V5/Tpxl; 1.
SWART; SM00198; SCP; 1.
SWART; SM00198; SCP; 1.
SEQUENCE 246 AA; 27956 MW; FB57702
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01-MAY-1997
01-JUN-2002
T05A10.5 pro
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InterPro; IPRO1283; Allryn_V5/Tpx1.
Pfam; PF00188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
PRODOM; PD000542; Allryn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
PROSTTE; PS01009; SCP, AG5_PR1_SC7_1; 1.
PROSTTE; PS01009; SCP, AG5_PR1_SC7_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE-99069613; PubMed-9851916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (NOV-1995) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               investigating biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome sequence of the nematode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                  59;
                                                                                                                                                               Similarity 27.: 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       282:2012-2018(1998).
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MRTMVYDCTLEEKAYKSAEKC-----SEEPSSEEENVDVFSAAT---LNIPLEAGNSWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAPCSRCSDYG-AGVTCDDDWQNLLCI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VYNK-----NGKTSNIANMVWDSHDKLGCAVVDCSGKTHVVCQYGPEAKGDGKTIYEE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEEKAYKSAEKC--SEEPSSEEEN--VDVFSAATLN----IPLEAGNSWWSEIFELRGK 100
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                                                                       LCQAPSMVKDDGGSFQCDNSLVSDVTRNFTLEQHNFYRSRLAKGFEWNGETNTSQPKASQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GNPCTNNEDCKCTNCVCSRD--EALCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IEENTMNFAKKCVFAHNSYSESNNWGQNLYMTSILNQNKTVAAAESVDLWFDEL-QQNGV
                                                                                                                  LCQQREKLDDD------KTSK
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2 (TrEMBLiel. )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nematoda; Chromadorea; rinae; Caenorhabditis.
                                                                                                                                                                                       21.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.5%; Score 214;
28.0%; Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03,
21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28;
                                                                                                                                                                  26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                       Score 209.5; DB 5; Pred. No. 1.2e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                          FB5770261350DE54 CRC64;
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                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhabditida; Rhabditoidea;
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                                                                                                                                                                  Indels
                                                                                                                                                                                                             Length,
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                                                                                                                                                               Gaps
                             91
                                                                          88
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Best Local S
Matches 55
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045132;
01-JUN-1998
01-JUN-1998
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1998 (TREMBLrel. 06, Created)
01-JUN-1998 (TREMBLrel. 06, Last sequence update)
01-JUN-2002 (TREMBLrel. 21, Last annotation update)
Putative secretory protein precursor.
HC40
G9BIQ4 PRELIMINARY; PRT; 491 AA.
G9BIQ4:
G9BIQ4:
G1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Activation associated secreted protein-like protein (Fragment).
Cooperia punctata.
Cooperia Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Trichostrongyloidea; Cooperiidae; Cooperia.
NCBI_TaxID-96640;
[1]
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SEQUENCE
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Submitted (FEB-1998) to the EMBL/GenBank/DDBJ
EMBL; AF047417; AR003562.1;
InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam; PF00188; SCEP; 1.
PFAMYS; PR001887; V5/TPXLIKE.
PRINYS; PR00187; V5/TPXLIKE.
PRINYS; PR000542; Allrgn_V5/Tpx1; 2.
SMART; SM00198; SCEP; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haemonchus contortus (Barber pole worm).
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Trichostrongyloidea; Haemonchidae; Haemonchinae; Haemonchus.
NCBI_TaxID-6289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AKGDGKTIYEEGAPCSRCSDYGAGVTCDDDWQNLLCI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEIFE-----LRGKYYNKNGKT-SNIANMYWDSHDKLGCAYYDCSGKTHYVCQYGPE 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIKMEYDCMLERFAQNWANNCVFAHSAHYERPNQGQNLYMSSFSNPDPRSLIHTAVEKWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VTCDDDWQNLLCI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNIANNYWDSHDKLGCAVVDC-SGKTHVVCQYGPEAKGDGKTIYEEGAPCSRCSDYGA-G 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FGLNTAAMLKRWGNNMHMMSKANNKTEAAAEAVAAWFGDLQKYGVPENNVFTNNVYTTL 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EEPSSEE-----ENVDVFSAATLN---IPLEAGNSWWSEIFEL---RGKVYNKNGKT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MTDEARKMFVDKHNEYRSLIAKGQAKGKPGQFAPKAARMMKVNYDCDVEANAMEWSKTCT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SKYSQLAWQSSDRIGCVVVPCWSSWTVVVCEYNPGGDLPGEAIYDVGDPCTKDADCQCPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCSRD--EALCY 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1
19
459 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.9%; Score 208; DB 5; Length 459, ilarity 28.5%; Pred. No. 3.6e-11; Conservative 36; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 POTENTIAL.
459 PUTATIVE SECRETORY PROTEIN.
50924 MW; 88FAC09A01FCA57B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Q19348
ID Q1934
AC Q
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O19348
O1948;
O1-0V-1996 (TrEMBLrel. 01, Cr
O1-0V-1998 (TrEMBLrel. 21, Lr
O1-0V-1998 (TrEMBLrel. 21, Lr
O1-0V-2002 (TrEMBLrel. 21, Lr
O1-0V-3 protein.
JR F11C7.3 protein.
SN F11C7.3 protein.
OS Canorhabditis elegans.
OS Canorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda
OC Eukaryota; Metazoa; Nematoda
OC Rhabditidae; Peloderinae; Cr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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Best Local S
Matches 57
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A Yarsuda A.P., Eysker M., Vieira Bressan M.C.R., De Vries E.;
T "Analysis of a family of activation associated secreted proting to the proting of Cooperia punctata,"
I submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP352702; AAK35187.1;
R EMBL; AP352702; AAK35187.1;
R Interpro; IPR001283; Align_V5Tpx1.
R Interpro; IPR001283; P_rich_extensn.
R Ffam; PF00188; SCF; 1, 11cn_v5Tpx1.
R PRINTS; PR00187; V5TPXLIKE.
R PRINTS; PR00837; V5TPXLIKE.
R PROSITE; PR00837; V5TPXLIKE.
                                                                                                                                                                                                                         REPUBLICE FROM N.A.

32 STRAIN-BRISTOL N2;

33 Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,

34 Wilson R., Ainscough R., Connell M., Copsey T., Cooper J., Coulson A.,

35 Author R., Ainscough R., Lonell M., Copsey T., Cooper J., Coulson A.,

36 Anfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,

37 Author M., Cear S., Du Z., Durbin R., Favello A., Fulton L.,

38 A Granton M., Geren P., Hawkins T., Hillier L., Jer M., Johnston L.,

39 A Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,

30 A J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,

30 A Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,

30 A Lightning J., Lloyd C., Mcmurray A., Mortimore B., Sounkeen R.,

30 A Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,

31 A Smaldon N., Smith A., Sonnhammer E., Staden R., Waterston R.,

32 A Matson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;

33 Matson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;

34 Cara C., Mortimore M., Waterston R.,

35 Matson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;

36 Cara C., Mortimore M., Waterston R.,

37 Cara C., Mortimore M., Waterston R.,

38 Matson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;

38 Cara C., Materston R.,

39 Cara C., Materston R.,

30 Cara C., Materston R.,

30 Cara C., Materston R.,

31 Cara C., Materston R.,

32 M. Of Contiguous nucleotide sequence from chromosome III of C.,

31 Cara C., Materston R.,

32 M. Of Contiguous nucleotide sequence from chromosome III of C.,

31 Cara C., Materston R.,

32 M. Of Contiguous nucleotide sequence from chromosome III of C.,

32 M. Of Contiguous nucleotide sequence from chromosome III of C.,

33 Cara C., Materston R.,

34 Cara C., Materston R.,

35 Cara C., Materston R.,

36 Cara C., Materston R.,

37 Cara C., Materston R.,

38 Cara C., Materston R.,

38 Cara C., Materston R.,

39 Cara C., Materston R.,

30 Cara C., Materston R.,

30 Cara C., Materston R.,

31 Cara C., Materston R.,

31 Cara C., Materston R.,

31 Cara C.,
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                   Nature | Nat
                                                                                                                                                                                   elegans.";
Nature 368:32-38(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KNGKTSNIANMYWDSHDKLGCAVVDCSGKTHVVCQYGPEAKGDGKTIYEEGAPCSRCSDY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ICSLNNGMTDVIRKIFLDKHNEYRSLVARGGAKDPRTGQTIPKATRMLKMSYDCEAEDYA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KCNGCTCST--TESLCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GA-GYTCDDDWQNLLCI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RDTDSVHYSQILWQDSYKIGCAVAWCQSMTWVACAYNPAGNNYGSQIYEQGEPCKRNQDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nematoda; Chromadorea; Rhabditida; Rhabditoidea; rinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 207.5; DB 5; Length Pred. No. 4.4e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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Johnston L.,

Coulson A.,

85;

Indels

193

491; 25;

SOR DE RECEPTION D

PF00188; SCP;

STRAIN-N2 BRISTOL; SEQUENCE FROM N.A.

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SEQUENCE FROM N.A.

GRO B., Allen R., Maier T., Davis E.L., Baum T.J., Hussey R.S.;
GRO B., Allen R., Maier T., Davis E.L., Baum T.J., Hussey R.S.;
"Molecular Characterization and expression of two venom allergen-like secretory proteins from Heterodera glycines.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AF714388; AMA60209.1;
InterPro; IPR001283; Allrgn_V5/Tpx1.
InterPro; IPR001230; Prenyl_site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00188; SCP; 1.
ProDom; PD000542; Allign_V5/Tpx1; 1.
PROSITE; PS00294; PRENYLATION; UUKNOWN_1.
SEQUENCE 215 AA; 23176 MW; FC200DDFCA8C8BB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (DEC-1998) to the EMBL/GenBank/DDBJ EMBL; U42839; AAC69015.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heterodera glycines (Soybean cyst nematode).
Eukaryota: Metazoa: Nematoda; Chromadorea: Tylenchida; Tylenchina:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0837; V5TPXLIKE.

Probem; PD000542; Allrgn_V5/Tpx1; 2.

SMART; SM00198; SCP; 2.

PROSITE; PS00294; PRRNYLATION; UNKNOWN 1.

SEQUENCE 425 AA; 46323 MW; 9E7233BBA7340EEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
[3]
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MBL; AF112356; AAD27559.1;

INTERPO; IPR001233; Allrgn V5/Tpx1.

InterPro; IPR001230; Prenyl_site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154 GAPCSRCSDYGAGVTC 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          342 DNILTQAVFDRG--VGHYTQMAWEGTTEIGCFVENCPTFTYSVCQYGPAGNYMNQLIYTK 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 282 EANARTWAKGCLYQHSTSAQRPGLGENLYMISINNMPKIQTAEDSSKAWWSELKDFGVGS 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         222 FTMCPSVTDQSDQARQNFLDTHNKLRTSLAKGLEADGIAAGAFAPMAKQMPKLVKYSCTV 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97 ---LRGKVYNKNGKTSNIANMVWDSHDKLGCAVVDCSGKTHVVCQYGPEAKGDGKTIYEE:153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 EEKAYKSAEKCSEEPSSEEE----NVDVFSAATLNIPL----EAGNSWWSEIFE---- 96
73 DVFSAATL---NIPLEAGNSWWSEI--FELRGKV-----YNKNGKTSNIANMVWDSHDK 121
                                                                                                                                          25 HNGYRAAFAR---NYKTSKMRT-----MVYDCTLEEKAYKSAEKCSEEPSSEE---ENV 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 YSLCQQREKLDDDMREWFTELHNGYRAAFARNYKTSKM-----RTMYYDCTL 50
                                                                              HNNYRSQLAKGTADNKSGKMPAGSNLIQQKYDSNIESVAQKWANGCSMSHSGSSGMGENL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSPCTADADCPGTQTC 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heteroderidae; Heteroderinae; Heterodera
                                                                                                                                                                                                                    19.0%; Score 189.5; DB 5; Length 215; 30.8%; Pred. No. 7.5e-10; tive 29; Mismatches 61; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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RESULT 15

OPEPN
ID OPEPN
AC OPEPN
AC OPEPN
AC OPEPN
AC OPEPN
DT 01-MA
DT 01-MA
DT 01-MA
DT 01-MA
CT 0
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04493
ID 04493
AC 04493
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-G
OC Eukar
OC Oncho
OC Eukar
OC NCBI_
RN [1]
RN [1]
RN [1]
RR STRAI
RA MCCAT
RA MCCAT
RH SNDM1
DR HSSP;
DR Inter
DR Pfam;
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Best Local Similarity 27.9%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-SIERRA LEONE;
MCCarthy J.S., Hopkins R.M.;
Submitted (JANN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF042087; AAB97282.1; -.
HSSP; P04284; ICFE.
InterPro; ITPR001283; A11rgn_V5/TpX1.
Pfam; PF00188; SCP; 1.
ProDom; PD000542; A11rgn_V5/TpX1; 1.
SMART; SM00198; SCP; 1.
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9GPN4;
                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TIEMBLIE1. 16, Created)
01-MAR-2001 (TIEMBLIE1. 16, Last sequence update)
01-JUN-2002 (TIEMBLIE1. 21, Last annotation update)
Activation-associated secreted protein-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1998 (TREMBLE). 06, Created)
01-JUN-1998 (TREMBLE). 06, Last sequence update)
01-JUN-2002 (TREMBLE). 06, Last sequence update)
01-JUN-2002 (TREMBLE). 21, Last annotation update)
Vespid allergen antigen homolog.
Onchocerca volvulus.
Eukaryota, Metazoa, Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Onchocerca.
similar to vespid venom antigen
                          SEQUENCE FROM N.A.
MEDLINE-20416487; PubMed-10960168;
Tawe W., Pearlman E., Unnasch T.R., Lustigman S.;
Tawe W., Pearlman E., Unnasch T.R., Lustigman S.;
"Angiogenic activity of Onchocerca volvulus recombinant proteins
                                                                                                                                                                                                                                                                                              Onchocerca volvulus.
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Onchocercidae; C
NCBI_TaxID=6282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      044931;
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                                                                                                                                                                                                                    NCBI_TaxID=6282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196 QGSPCKVNKHCRTKKCS 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153 EGAPC-----SRCS 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 SNKLTSSVASQDVLHFTQMAWGKTHKVGCGIAMHCDDGEAFIVVCHYAPRGNTIGELIYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 NGK-TSNIAN------MVWDSHDKLGCAVV---DCSGKTHVVCQYGPEAKGDGKTIYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 IGCAMARCPSSTWKTWVVCNYKEAGNFLNQPVYKKGAACSKCSDYN-GATCD 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 LGCAVVDC---SGKTHVVCQYGPEAKGDGKTIYEEGAPCSRCSDYGAGVTCD 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 REKLDDDMREMFTELHNGYRAAFAR-NY-----KTSKMRTMVYDCTLEEKAYKSAE 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 YMTSSSTISEADALKQACDMWWAELKQFGFQSSLVLDMAQFNKG--IGHWSQQAWASTAQ 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 QCIFGYSPENQREGYGENIYALGLPKDYEYFNTSAALFAIE---SWWTEL--IRSYRNNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 KC--SEEPSSEEE------NVDVFSAATLNIPLEAGNSWWSEIFELRGKVYNK 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 RGKLTSLORDIIVDEHNKYRSRLVKGNFANKDGNLMPKGKNMMEMEWDCELEISAQNWAD 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                               Onchocerca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.8%; Score 187; DB 5; Length 22 27.9%; Pred. No. 1.3e-09; ative 29; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224 AA.
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Query Match Best Local S

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Q96317

PRELIMINARY;

RESULT 13
096317
ID 09631
AC 09631
DT 01-DE
DT 01-DE
DT 01-DE
DT 01-DE
DT 01-TD
DE Vap-1
OS Heter
OC Eukar
OC Tylen
OX NCBI.
(1)
RN 11|
RN SEQUE
RN GAO B
RT SEQUE
RA GAO B
RT SECUE
RT SUBM!
DR Pfam:
DR Inter
DR Inter
DR Inter
DR Pfam;
DR

NCBI_TaxID-51029;

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38

Query Match Best Local S Matches 53

Similarity

Conservative

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RESULT
OPERATOR

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                                                                                                                                                                                                                    Query Match
Best Local S
Matches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MO1. Blochem. Parasitol. 109:91-99(2000).
EMBL; AF314563; AAG40311.1; .
InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam; PF00188; SCC; 1.
PRLNTS; PR00837; V5TPXLIKE.
PRODOM; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCC; 1.
SMART; SM00198; SCC; 1.
SEQUENCE 224 AA; 25253 MW; 8AF47A01522F
                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CP-ASPVAR-6;
STRAIN-CP-ASPVAR-6;
Yatsuda A.P., Eysker M., Vieira Bressan M.C.R., De Vries
"Analysis of a family of activation associated secreted
homologs of Cooperia punctata.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF352699; AAX35184.1;
HSSP; P04284; ICFE.
InterPro; IPR001283; Allrgn_V5/Tpx1.
                                                                                                                                                                                                                                                                                                                          Pfam; PF00188; SCP; 1
PRINTS; PR00837; V5TPXIIKE.
Probom; PD000542; Allirgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09BIQ7
09BIQ7;
                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cooperia punctata.
Eukaryota; Metazoa; Nematoda;
Trichbstrongyloidea; Cooperiid
NCBI_TaxID-96640;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-UN-2001 (TrEMBLrel. 17, Created)
01-UN-2001 (TrEMBLrel. 17, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Activation associated secreted protein-like protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQUENCE FROM N.A.
104 K----NGKTSNIANNVWDSHDKLGCAVVDC--SGKTHVVCQVGPBAKGDGKTIYEEGAP 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198
                                                     92 VKTCKGGHSPFSVLKGRGQNIWAITVPNLDKAEAAKRSV----DDWYIELTKYGITADN 146
                                                                                                    88
                                                                                                                                        32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 REKLDDDMREMFTELHNGYRAAFAR-NYKTS-----KMRTMVYDCTLEEKAYKSAE
                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                     CQQREKLDDDMREMFTELHNGYRAAFARNY-----KTSKMRTMVYDCTLEEKAYKS 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                             AEKC--SEEPSS------EEENVDVFSAATLNIPLEAGNSWWSEIFELRGKVYN 103
                                                                                                                                   CTLNNGMTDDVRQVFLDKHNEYRQLVARGEAQNKTGFAPKAARIHRLRYDCDLEAHVMEH 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RPCKTDRD 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APCSRCSD 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            K-----NGKTSNIANMVWDSHDKLGCAV-VDC-SGKTHV-VCQYGPEAKGDGKTIYEEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KYTSIVANRGVSNFTQLAWGKTYKVGCGIATHCDGGKAFVAVCQYNPGGNTMGESIYEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QCVSGNSPKDRRGRIGENVYTQRSDTSVAVYGTSGIMIALE---SWWVELTRSYKNNPSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RGKLTPOYREKIVREHNRLRSKLAKGTYKNSAGKWMPKGKNMMEMKWDCELELMAQRWAD
                                                                                                                                                                                                                                                                                             231 AA;
                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                           25824 MW; C5225C9AA17AAD00 CRC64;
                                                                                                                                                                                                                                   18.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nematoda; Chromadorea; Rhabditida; Strongylida; Cooperlidae; Cooperla.
                                                                                                                                                                                                                    27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20;
                                                                                                                                                                                                                                   Score 182;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 184; DB 5;
Pred. No. 2.6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8AF47A01522F5C3A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231
                                                                                                                                                                                                                                 DB 5;
4.le-09;
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                                                                                                                                                                                                             86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73;
                                                                                                                                                                                                                                                   Length 231;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      De Vries E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                             36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38;
                                                                                                                                                                                                           Gaps
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  RRR OCCORDITAL
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RESULT 18
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Best Local Similarity
Matches 53; Conserv
                                                                         Cooperia punctata.
Eukaryota; Metazoa; Ne
Trichostrongyloidea; (
NCBI_TaxID=96640;
                                                                                                                                             Q9BIQ8 PRELIMINARY; PRT; 248 AA.
Q9BIQ8;
Q1-JUN-2001 (TIEMBLIE1. 17, Created)
01-JUN-2001 (TIEMBLIE1. 17, Last sequence update)
01-JUN-2002 (TIEMBLIE1. 21, Last annotation update)
Activation associated secreted protein-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001
01-JUN-2001
01-JUN-2002
  SEQUENCE FROM N.A.
STRAIN-CP-ASPVAR-7;
Yatsuda A.P., Eyske
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9BIQ6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CP-ASPVAR-5;
Yatsuda A.P., Bysker M., Vieira Bressan M.C.R.,
*Analysis of a family of activation associated s
homologs of Cooperia punctata.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ de
EMBL; AP35700; AAS5185.1;
HSSP; P04284; ICFE.
HSSP; P04284; ICFE.
HSSP; P04284; ICFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cooperia punctata.

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Activation associated secreted protein-like protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CBI_TaxID=96640;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                        157
                                                                                                                                                                                                                                                                                                                                                                                                                            164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                104
                                                                                                                                                                                                                                                                                                                                                    224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 VAKCKGGHSTFDVLKGRGQNIWAITVPNLDKAEAAKRSV-----DDWYIELTKYGITADN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 KISIDNAAKTGHYSQVVWQKSNRLGCAAVSCPEQRKLFVGCEYLPGGNTLRHLIYDIGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00188; SCP; 1.
S; PR00837; V5TPXLIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 CSRCSDYGAGVTCDDDWQNLLCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 AEKCSEEPSSEE------ENVDVFSAATLNIPLEAGNSWWSEIFELRGKVYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49
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                                                                                                                                                                                                                                                                                                                                                    CKRDEDCKCS-SCRCSTQLSMCI 245
                                                                                                                                                                                                                                                                                                                                                                                      CSRCSDYGAGVTCDDDWQNLLCI 179
                                                                                                                                                                                                                                                                                                                                                                                                                          KISIDNAAKTGHYSQVVWQKSNRLGCAAVSCPEQRRLYVGCEYWPGGNTLRHLIYDIGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                              K-----NGKTSNIANMVWDSHDKLGCAVVDC--SGKTHVVCQYGPEAKGDGKTIYEEGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTLDNGMTDEARQVFLDKHNEY RQLVARGEAQNKTGLAPPAARMLKLRYDCDLEAHVMEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CQQREKLDDDMREMFTELHNGYRAAFARNYKTSK-----MRTMYYDCTLEEKAYKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CKRDEDCKCS-SCRCSTQLSMCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 AA; 27528 MW; ABF932E60DB67411 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TIEMBLIel. 17, Created)
(TIEMBLIel. 17, Last sequence update)
(TIEMBLIel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
  Eysker M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Allrgn_V5/Tpx1; 1
                                                                                                                    Nematoda;
                                                                                              Nematoda; Chromadorea; Rhabditida; Cooperiidae; Cooperia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.1%; Score 180; DB 5; 26.1%; Pred. No. 6.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cooperiidae; Cooperia
  Vieira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ databases
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  Bressan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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M.C.R.,
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  De
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  Vries
                                                                                                                                                      (Fragment).
                                                                                                                  Strongylida;
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SO DR DR RT

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RESULT 19
09JJ56
AC 09JJ5
DT 01-0C
DT 01-0C
DT 01-CC
DT 0
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Best Local S
Matches 53
                                                                                   Query Match
Best Local S
Matches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *Analysis of a family of activation associated secreted protein (ASP) homologs of Cooperia punctata."; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AB352698; ARAS5183.1; *.

HSSP: P04284; ICFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam; PF00188; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             091156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART;
                                                                                                                                                                                                                                                                                                                                                  Submitted (JUL-2000)
EMBL; AB046537; BAB0:
HSSP; P04284; 1CFE.
MGD; MGI:1921366; 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Cysteine-rich protease inhibitor.
1200009H11RIK OR CRIPI.
                                                                                                                                                                                                      PRINTS; PRO0837; VSTPXLIKE.

PRODOM; PD000542; Allrgn_V5/Tpx1; 1.

SMART; SM00198; SCP; 1.

PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.

PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
                                                                                                                                                                  Protease.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENDUBLOE FROM N.A.

'Identification of novel mouse cycteine-rich protease inhibitor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58
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SM00198; SCP; 1
R 1
                                                                                                                                                                                                                                                                                                              PF00188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 COOREKLDDDMREMFTELHNGYRAAFARNYKTSK-----MRIMVYDCTLEEKAYKS 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 Similarity 26.1
53; Conservative
                                       13 LDDDMREMETELHNGYRAAFARNYKTSKMRTMVYDCTLEEKAYKSAEKC----SEEPSSE
21 LTEDEKQTMVDLHNQYRAQVSP--PASDMLQMRWDDELAAFAKAYAQKCVWGHNKERGRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AEKCSEEPSSEE-----ENVDVFSAATLNIPLEAGNSWWSEIFELRGKVYN 103
                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTLDNGMTDEARQVFLDKHNEYRQLVARGEAQNKTGLAPPAARMLKLRYDCDLEAHVMEH 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CKRDEDCKCS-SCRCSTQLSMCI 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KISIDNAAKTGHYSQVVWQKSNRLGCAAVSCPEQRRLYVGCEYWPGGNTLRHLIYDIGEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CSRCSDYGAGVTCDDDWQNLLCI 179
                                                                                                                                                                                                                                                                                                                          1921366; 1200009H11R1k.
1921366; 1200009H11R1k.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 AA; 27558 MW; A7EDA83B9BEF7481 CRC64;
                                                                                                                                                                    489 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                       000) to the EMBL/GenBank/DDBJ databases. BAB03398.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Allrgn_V5/Tpx1; 1.
                                                                                                                                                                      52676 MW; 01C207BE12E3CB9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.9%; Score 178; Di
26.1%; Pred. No. 1e-C
Live 27; Mismatches
                                                                                                         17.9%;
                                                                                     b; Score 178; DB
b; Pred. No. 2.4e-
25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     489
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                                                                                     DB 11; Length 48:
.4e-08;
.es 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₿
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                                                                                                                             Length 489;
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                                                                                          34;
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                                                                                          Gaps
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                 78
                                                   89
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Q9ET66
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                 RESULT 21
Q9N5N4
ID Q9N5N
AC Q9N5N
DT 01-OC
DT 01-OC
DT 01-OC
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4d
5d
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Best Local S
Matches 53
                 Q9N5N4
Q9N5N4;
Q1-OCT-2000
Q1-OCT-2000
Q1-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001281
Pfam; PF00188; SCP;
PRINTS; PR00837; V5
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PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
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                                                                                                                                                                                                 186 ENSIC 190
                                                                                                                                                                                                                                    174 QNLLC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 28.6
53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QNLLC 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     489 AA;
                   (TrEMBLrel. 15,
(TrEMBLrel. 15,
(TrEMBLrel. 21,
                                                                                                  PRELIMINARY;
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OPET66 PKELLE-----
QPET66 PKELLE-----
QPET66 PKELLE-----
OPET64 PT PROPERT PROPERTY PROPE
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SEQUENCE FROM N.A.

Jang J.S., Hahn Y., Chung J.H.;

Genemaic structure of murine cysteine-rich protease inhibitor gene.";

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AB046539; BAB03453.1;

EMBL, AB046539; BAB03453.1;

EMBL, AB046539; BAB03453.1;

InterPro; IPR001283; Allrgn_V5/Tpx1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 LGCAVVDC-----SGKTH-VVCQYGPEAKGDGKTIYEBGAPCSRCSDYGAGVTCDDDW 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 GENLFAITDEGMDVPLAVGN--WHEEHE----YYNFSTATCDPNOMCGHYTQVVWSKTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 EENVDVFSAATLNIPLEAGNSWWSEIFELRGKVYN-----KNGKTSNIANMVWDSHDK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 LTEDEKQTMVDLHNQYRAQVSP--PASDMLQMRWDDELAAFAKAYAQKCVWGHNKERGRR 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 LDDDMREMFTELHNGYRAAFARNYKTSKMRTMVYDCTLEEKAYKSAEKC----SEEPSSE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGCGSHFCETLQGVEEANIHLLVCNYEPPGNVKGRKPYQEGTPCSQCP---LGYSC----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGCGSHFCETLQGVEEANIHLLVCNYEPPGNVKGRKPYQEGTPCSQCP---LGYSC----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.9%; Score 178; DB 11; Length 489; 28.6%; Pred. No. 2.4e-08; tive 25; Mismatches 73; Indels 34;
Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                208 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Best Local S
Matches 52
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ da
EMBL; AC006655, AAF39876.1;

InterPro; IPR001283; Allrgn_V5/Tpx1.

Pfam; PF00188; SCP; 1

PRINTS; PR00837; V5TPXLIKE.

PRODOM: PR00837; V5TPXLIKE.

PR00837; V5TPXLIKE.

PR00837; V5TPXLIKE.

PR00837; V5TPXLIKE.

PR00837; V5TPXLIKE.

PR00837; V5TPXLIKE.

PR00838; V5TPXLIKE.

Strausberg R.;
Submitted (FEB-2002) to t
EMBL; BC022399; AAH22399,
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                            01-JUN-2002 (TERMBLrel. 21, Created)
01-JUN-2002 (TERMBLrel. 21, Last sequence update)
01-JUN-2002 (TERMBLrel. 21, Last anotation update)
11-JUN-2002 (TERMBLrel. 21, Last anotation update)
14-JUN-2002 (TERMBLRel. 21, Last anotation update)
15-JUN-2002 (TERMBLRel. 21, Created)
16-JUN-2002 (TERMBLRel. 21, Last sequence update)
16-JUN-2002 (TERMBLRel. 21, Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QSTCB8
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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STRALM-BRISTOL N2;
Madsen C., Tin-Wollam A., Ke
"The sequence of C. elegans
Submitted (MAR-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H10D18.4
H10D18.4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DAHNKLRSATAQGSYVAAGTQEPSASNMRKIVWDETVAAAAQEYAEGCPDDHSGTSYGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACSE---DASCEQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RCSDYGAGVTCDDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---NIANMYWDSHDKLGCAVVDCSG------KTHVVCQYGPEAKGDGKTIYEEGAPCS 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LYWSWSSSAPSSLDKFGVA-----ASNSWESE-----FQKYGWTSTFLDEAGFAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nematoda; Chromadorea; Rhabditida; Rhabditoidea; rinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.8%;
                                              9.1;
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ns cosmid H10D18.";
he EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 167; DB
; Pred. No. 8.9e.
22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
                                                   EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       415
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1.9e-08;
les 58;
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                                                                                        databases
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Query Match 15.8%; Score 158; DB 4; Best Local Similarity 25.5%; Pred. No. 1.8e-06; Matches 53; Conservative 31; Mismatches 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 53
                                                                                                       Submitted (JAN-2002) to the EMBL/GenBa EMBL; APT42573; AAG43287.1; -.. EMBL; APZ329197; AAK16495.1; -.. EMBL; BC020514; AAH20514.1; -.. HSSP; P04284; ICFE. InterPro; IPR001283; All:gn_V5/Tpx1. InterPro; IPR004043; LCCL_dom. Pf0n; PF00188; SCP; 1. PRINTS; PR00837; V5TPXLIKE. ProDom; P000542; All:gn_V5/Tpx1; 1. SMART; SM00198; SCP; 1. SMART; SM00198; SCP; 1. PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1 PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1 SEQUENCE 500 AA; 56888 MM; 203BIDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9H336 PRELIMINARY; PRT; 500 AA.
Q9H336;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-UN-2002 (TrEMBLrel. 21, Last annotation update)
Putative secretory protein precursor (Cocoacrisp).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

TESSTES-HEART, AND TESSTIS;
TISSUE-HEART, COLLINE-Racie L.A., Lavallie E.R., Gamer L., Rober Smith D.M., Collins-Racie L.A., Lavallie E.R., Gamer L., Rober Marigo V.A., Copeland N.G., Jenkins N.A., McCoy J., Tabin C.J.

"A novel cysteine-rich secreted protein (CRISP) family member, Cocoacrisp, provides insight into the process of septation in developing chicken midbrain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
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Submitted (J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE-OVARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhao Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-AORTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhao Y., Cao H., Jiang Y., Meng X., "Cloning and characterization of a t in human acorta.";
Submitted (APR-1999) to the EMBL/Ger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 QNLLC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 LGCAVVDCS-----GKTHV----VCQYGPEAKGDGKTIYEEGAPCSRCSDYGAGVTCDDDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 EENVDVFSAATLNIPLEAGNSWWSEIFELRGKVYNKNGKTSNIANM------VWDSHDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 LTDEEKRLMVELHNLYRAQVSPT--ASDMLHMRWDEELAAFAKAYARQCVWGHNKERGRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 LDDDMREMFTELHNGYRAAFARNYKTSKMRTMVYDCTLEEKAYKSAEKC----SEEPSSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 Similarity
53; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DEC-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            415 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204
                                                                                                          SCP_AG5_PR1_SC7_2; 1.
; 56888 MW; 203B1DC4DDA003CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1
45230 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ databases.
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Pred. No. 1.2e-06;
6; Mismatches 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      945069C1607D38E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . zhao x., Liu D., Ding
trypsin inhibitor-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vertebrata;
1; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72;
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                                                     Length 500;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Euteleostom1;
; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Roberts D.J.,
n C.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J.;
protein
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O97149 PRELIMINARY;
O97149;
O1-MAY-1999 (TrEMBLrel. 10,
O1-MAY-1999 (TrEMBLrel. 10,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Seltman A.K., Steel C.S., Ottesen E.A., Nutman T.B.;
Seltman A.K., Steel C.S., Ottesen E.A., Nutman T.B.;
Filerification of potentially protective antigens in human lymphatic fileriasis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam; pF00188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wuchereria bancrofti.
Eukaryota; Metazoa; Nemato
Onchocercidae; Wuchereria.
NCBI_TaxID-6293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  espid allergen antigen homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 KLDDDMREMFTELHNGYRAAFARNY-----KTSKMRTMVYDCTLEEKAYKSAEKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 27.2
50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        --SEEPSSEE----ENVDVF--SAATLNI----PLEAGNSWWSEIFELRGKVYNKNGKTS 109
                                                                                                                                                                                                                                                                                                                        DVSRQGVLHFTQMAWGKTHKIGCGIATNCDGGRTLITICHYSPAGNILKNLIYELGEPCK 20:
                                                                                                                                                                                                                                                                                                                                                                         NIA-----NMVWDSHDKLGCAV-VDC-SGKTHV-VCQYGPEAKGDGKTIYEEGAPCS 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QLTPQQRKDIVRQNNKFRSLLIRGKLKNRNGTYMPRGKNMLQLTWSCQLENSAQRWANQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPKGNWWGHAPYKHGRPCSACPPSFGGG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WAESCLWEHGPAS-----LLPSIGQNLGAHWGRYRPPTFHVQSWYDEVKDFSYPYEHEC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGEWWIAKORGKRAITDNDMOSIL-DLHNKLR---SOVYPTASNMEYMTWDVELERSAES 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPEAKGDGKTIYEEGAPCSRC-SDYGAG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NPYCPFRCSGPV-----CTHYTQVVWATSNRIGCAINLCHNMNIWGQIWPKAVYLVCNY 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----FELRGKVYNKNGKTSNIANMVWDSHDKLGCAVVDCSG-----KTHVVCQY 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAEKCSEE--PSSEEENVDVFSAATLNIPLEAG-----NSWWSEI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGDYSLCQQREK---LDDDMREMFTELHNGYRAAFARNYKT-SKMRTMVYDCTLEEKAYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TremBLrel. 13, Created)
(TremBLrel. 13, Last sequence update)
(TremBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24617 MW; 7439F5DB1C96E978 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nematoda; Chromadorea; Spirurida; Filarioidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 157; DB
Pred. No. 8.2e-
26; Mismatches
Created)
Last sequence update)
                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                      220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34;
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   Q20608

Q20608

ID Q2060

DT Q1-NC
DT Q1-NC
DT Q1-NC
DT Q1-NC
DT Q1-NC
CAPEC
OC CAPEC
OC RhAbd
OX NCSI.
RN [1]
RP SEQUE
RA Bayne
RL Submil
RN [2]
RP Genc
RT Gnce;
RA MEDL;
RA
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Best Local S
Matches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           020608 PRELIMINARY; PRT; 207 AA.
020608; (TIEMBLrel. 01, Created)
01-NOV-1996 (TIEMBLrel. 01, Last sequence update)
01-NOV-1996 (TIEMBLrel. 21, Last annotation update)
P49E11.9 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001283; Allrgn_V5/Tpx1.

Pfam; PF00188; SCP; 1.

PRINTS; PR00837; V57PXLIKE.

PT0D0m; PD000542; Allrgn_V5/Tpx1; 1.

SMART; SM0128; SCP; 1.

SEQUENCE 220 AA; 24640 MW; 84314:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                        InterPro; IPRO01283; Allrgn_V5/Tp:
Pfam; pP00188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
ProDom; pD000542; Allrgn_V5/TpX1;
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hopkins R.M., McCarthy J.S.; "Cloning of the Wuchereria bancrofti venom allergen homolog."; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AF109794; ADD16985.1; "... HSSP; P04284; ICFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2002 (TrEMBLrel.
Vespid allergen antigen
                                                                                                                                                       "Genome sequence of the nematode C.elegans: A platform investigating biology."; Science 28:2012-2018(1998).

EMBL: 270308; CAA94348.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F49E11.9
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Eukaryota; Metazoa; Nematoda; Chromadorea;
Onchocercidae; Wuchereria.
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-99069613; Pubmed-9851916;
                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. Baynes C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   159 RCSD 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 DVSRQGVLHFTQMAWGKTHKIGCGIATNCDGGRTLITICHYSPAGNILKNLIYELGEPCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 NIA-----NMVWDSHDKLGCAV-VDC-SGKTHV-VCQYGPEAKGDGKTIYEEGAPCS 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83 VFGHSPRNQRQGIGENVYAYWSSASVENLRKTAGTEAGKSWWSELPELY-KHNPSNNLTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 -- SEEPSSEE----ENVDVF--SAATLNI----PLEAGNSWWSEIFELRGKVYNKNGKTS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 KLDDDMREMFTELHNGYRAAFARNY-----KTSKMRTMVYDCTLEEKAYKSAEKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 Similarity 27.: 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KDGD 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QLTPQQRKDIVRQNNKFRSLLIRGKLKNRNGTYMPRGKNMLQLTWSCQLENSAQRWANQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.6%; Score 156; DB 5; Length 27.2%; Pred. No. 1e-06; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24640 MW; 84314558E31540D4 CRC64;
      21932 MW;
                                                                                                                                 Allrgn_V5/Tpx1
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      5D6F6E96794B4C1A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
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RESULT 24
Q9UBO3
ID Q9UBO
AC Q9UBO
DT 01-MA
DT 01-MB
DT 01-MB
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CO Onche
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01-MAY-2000 01-MAY-2000 01-JUN-2002

Q90B03; Q90B03

RESULT 25 097149 ID 09714 AC 09714 DT 01-MA DT 01-MA

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83 62 Query Match Best Local S Matches 50

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202 159 142

KDGD 205 RCSD 162

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RESULT 28
Q20609
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0937417
ID
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Best Local
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0837; V5TPXLIKE.

PTODOMS; PD000542; Allrgn_V5/Tpx1; 1.
SMARF; SM0138; SCP; 1.
SEQUENCE 213 AA; 23979 MW; ADD561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              093747 PRELIMINARY;
093747;
01-FEB-1997 (TIEMBLIEL 02,
01-FEB-1997 (TIEMBLIEL 02,
01-JUN-2002 (TIEMBLIEL 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       investigating biology.";
Science 282:2012-2018(1998).
EMBL; 270308; CA94351.1; -.
InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam; PF00188; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAR-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome sequence of the nematode C.elegans: A platform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F49E11.4 protein.
                                                                                               150
                                                                                                                                   122
                                                                                                                                                                            91
                                                                                                                                                                                                                   72
                                                                                                                                                                                                                                                         31
                                                                                                                                                                                                                                                                                      24 LHNGYRAAFA-----RNYKTSKMRTMVYDCTLEEKAYKSAEKCSEEPS---SEEEN 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197 TKCD
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                                                                                        VGCGYSKCAVGTPEQTMVVVCRYFQKGNIEGEPIYNEGETCTKCPE 195
                                                                                                                       LGCAVVDCSGKTH-----VVCQYGPEAKGDGKTIYEEGAPCSRCSD 162
                                                                                                                                                              IFWHFSSSLSTPEQYATLAPQKWWNE-FETNGWDSLIYNHASQRFQIGHAVQMAWHTTSK 149
                                                                                                                                                                                                    VDVFSAATLNIPLE----AGNSWWSEIFELRG---KVYNKNGKTSNIAN---MVWDSHDK 121
                                                                                                                                                                                                                                               VHNEFRSQLALGQLSFRGVKKPSASMMRKISWSKKLTNAATKFAETCPKNHSVVMNTGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AWANTSSIGCGVKNCGRDASMRNMNKIAVVCQYSPPGNTMGRPIYKEGTTCSSCS---GS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VWDSHDKLGCAVVDCS------GKTHVVCQYGPEAKGDGKTIYEEGAPCSRCSDYGAG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YGENLYWSWTSADVGSLDSYG---EIAAAAWEKEFQDFGWKSNAMDTTLFNSGIGHATQM
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                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                23979 MW; ADD56E2B33A9DD8A CRC64;
                                                                                                                                                                                                                                                                                                                                                         15.3%; Score 153;
27.1%; Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                        29;
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Last sequence update)
Last annotation update)
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1.8e-06;
hes 64;
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nes 71;
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                                                                                                                                                                                                                                                                                                                                   28;
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                                                                                                                                                                                                                                                                                                                                 7;
RESULT 29

1D 01685
AC 01685
AC 01685
AC 01685
DT 01-MA
DT 01-MA
DT 01-MA
DT 01-MA
OV-AS
ON OV-AS
ON ONCHO
OX NCBL
RN [1]
RN [1]
RX MEDLI
RA TAWE
RT *Angil
RI 81mil
RL M01.
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O16854; O15854; OTEMBLrel. 05, Created)

O1-JAN-1998 (TIEMBLrel. 05, Created)

O1-MAY-2000 (TIEMBLrel. 13, Last sequence update)

O1-JUN-2002 (TIEMBLrel. 21, Last annotation update)

E Activation-associated secreted protein-1.

OV-ASP-1.
ON-ASP-1.
Onchocerca volvulus.
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida NCBL-TaxID-6283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 51
  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-FOREST;
MEDILINE-2041648; PubMed-10960168;
Tawe W., Pearlman E., Unnasch T.R., Lustigman
"Angiogenic activity of Onchocerca volvulus re
similar to vespid venom antigen 5.";
Mol. Biochem. Parasitol. 109:91-99(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00837; V5TPXLIKE.
Probom; pD000542; Allrgn_V5/TpX1; 1.
SMARR; SM00198; SCF; 1.
SEQUENCE 212 AA; 23359 MW; 5A4DB40539CB708C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    020609;
020609;
01-NOV-1996;
01-NOV-1996;
01-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
Eukaryota; Metazoa; Nemat.
Rhabditidae; Peloderinae;
RCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .nvestigating biology.";
science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDLINE-99069613; PubMed-9851916;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 YKSAEKCSEEPSSEEENVD------VFSAATLNIPLEAGNSWWSEIFELRGKVYNK 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 FSFCETLCEFSETGKNYILSRHNYLRSQIALGKYVAGNSTKPSASNMMKLIWDTTLETTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 YSLCOOREKLDDDMREMFTELHNGYRAAFA-----RNYKTSKMRTMVYDCTLEEKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 24.5% Signature 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KSGETCSNCPD---GINCES--SIGECV 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEGAPCSRCSDYGAGVTCDDDWQNLLCI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NLLTEELFNSGIGHATQMAWATTNKIGCGISKCSSDSFGTQYVVVCLYSPAGNYIGMDIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NGKTSNIAN-----MVWDSHDKLGCAVVDCSGKTH-----VVCQYGPEAKGDGKTIY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QDYSTGCPTGHSASRANIGENMYWWTSPVVTQTDAELLGNRSANLWESE-FQRFG--WNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
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(TremBurel. 01, Last sequence update)
(TremBurel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.2%;
24.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nematoda; Chromadorea; Rhabditida; Rhabditoidea; rinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 152; DB 5; Leny...
Pred. No. 2.3e-06;
Pred. No. 2.3e-06; Indels
                                                                                                                                                                                                                   Chromadorea; Spirurida; Filarioidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212
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                                                    recombinant proteins
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Length 212;

40;

Gaps

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Best Local S
Matches 47
       Query Ma
Best Loc
Matches
                                                                                                                                                                                                                           Kaplan F., Ledoux P., Kassamali F.Q., Gagnon S., Post M., Koehler D., Deimling J., Sweezey N.B.;
"A novel developmentally regulated gene in lung mesenchyme: homology to a tumor derived tryssin inhibitor.";
Am. J. Physiol. 276:L1027-L1036(1999).
EMBL, AE109674; AAD16986.1;
InterPro: Terror.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           llbrary.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AF020586; AAB69625.2;
EMBL; P04264; ICFE.
InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam; PF00188; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9Z0U6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1999 (TEMBLEEL 10, Created)
01-MAY-1999 (TEMBLEEL 10, Last sequence update)
01-UN-2002 (TEMBLEEL 21, Last annotation update)
Late gestation lung protein 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpx1; 1.
SMARR; SM00198; SCP; 1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Joseph G.T., Lustigman S.;
Cloning and characterization of a cDNA clone, Ov B93 from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-FOREST;
                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139 MTWKVAGQGVLHFTQMAWGKTYKIGCGVATQCDGGRTLIVICHYSPGGNMVGEVIYHRGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65
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       52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 25.8
17; Conservative
                              Similarity
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          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCP_AG5_PR1_SC7_2; UNKNOWN_1.
c; 24510 MW; C089BFAE8869EBAB CRC64;
                                                                                       SCP_AG5_PR1_SC7_2; 1.
; 21907 MW; 5B6CC77515360BCE CRC64;
                         14.8%;
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Score 148; DB 11;
Pred. No. 4.6e-06;
2; Mismatches 61;
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Pred. No. 2.4e-06;
4; Mismatches 69;
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                                              Length 188;
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     Indels
     58;
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RESULT 32
Q18543
ID Q1854
AC Q1854
DT 01-NO
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Best Local S
Matches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       044932 PRELIMINARY;
044932;
01-JUN-1998 (TrEMBLrel. 0.
01-OCT-2000 (TrEMBLrel. 1.
01-JUN-2002 (TrEMBLrel. 2.
Vespid allergen antigen h
Q18543 PRELIMINARY;
Q18543;
01-NOV-1996 (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                        Murray J., Gregory W.F., Atmadja A.K., Maizels R.M.;
"Expression and immune recognition of Brugia malayi VAL-1, a homolog
of vespid venom allergens and Ancylostoma secreted proteins.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF042088; AAB97283.2;
EMBL; AF042088; AAB97283.2;
EMBL; AF934661; AAK12274.1;
InterPro; IFR001283; Allign_V5/Tpx1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brugia malayi.
Bukaryota; Metazoa; Nematoda;
Onchocercidae; Brugia.
NCBI_TaxID=6279;
                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-TRS LABS;

STRAIN TRS LABS;

"Cloning of the Brugia malayi VA homolog.";

Submitted (APR-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117
                                                                                                                                               118 -EAGKSWWSEL----PKLYKQNPSNNLTDDVARQGVLHFTQMAWGKTHKIGCGIATNCDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168
                                                                                                                                                               84 LEAGNSWWSEIFELRGKVYNK---NGKTSNIA-----NAVWDSHDKLGCAV-VDC-S 130
                                                                                                                                                                                                  62 MILLKWSCQLENSAQRWANQCVFGHSPRNQRQGIGENVYAYWSSESVEKLRNTAGT----
                                                                                                                                                                                                                   41 MRTMVYDCTLEEKAYKSAEKC--SEEPSSEE----ENVDVF------SAATLNIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53
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                                                                                                                                                                                                                                                    45;
                                                                                                                                                                                                                                                   Similarity 29.4
15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LHNGYRAAFARNY-KTSKMTHMYYDCTLEEKAYKSAEKCSEE--PSSEEENVDVFSAATL
                                                                                              GRTLIAICHYSPAGNMLKELIYELGEPCKTDSD
                                                                                                                    GKTHV-VCQYGPEAKGDGKTIYEEGAPCSRCSD 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G--C---RNNLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTNKIGCAVHTCRSMSVWGDIWENAVYLVCNYSPKGNWIGEAPYKHGRPCSECPSSYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NLAVHWGRYRSPGFHVQSWYDEV-----KDYTYPYPHECNPWCPERCSGAMCTHYTQMVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIPLEAG-----NSWWSEIFELRGKVYN-----KNGKTSNIANMVW
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                                                                                                                                                                                                                                                                                                          220 AA;
                                                                                                                                                                                                                                                                                                  ,24761 MW; F22F11AD7768FE65 CRC64;
                                                                                                                                                                                                                                                   14.8%; Score 148; DB 5; Length 220; 29.4%; Pred. No. 5.6e-06; tive 20; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06, Created)
15, Last sequence update)
21, Last annotation update)
homolog (Venom allergen ant
    Created)
                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chromadorea; Spirurida;
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                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                  117
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                                                                                                                                                 172
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Gaps

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Q9N3IJ

1D 09N3I

AC 09N3I

AC 09N3I

D9N3I

D1 01-OC

D7 01-OC

D7 01-OC

D7 01-OC

CELKAI

OC ELKAI

OC Rhabe

OC Rhabe

OC Rhabe

CO Rhabe

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RP SEQUE

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RN (11)

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RN (12)

RN (13)
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Best Local S
Matches 45
                                                                                                                                                                                                                                                                                                      Q9N313 PRELIMINARY; PRT; 246 AA.
Q9N311;
01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 26.9 kDa protein.
v51H7C.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                  Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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pfam; pr00188; SCP; 1.
prxNTS; pr00037; V5TPXIKE.
probom; p000542; Allrgn_V5/Tpx1; 1.
smarr; sM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
C39E9.2 protein.
C39E9.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z70307; CAA94335.1; -. HSSP; P04284; ICFE.
  SEQUENCE FROM N.A
STRAIN-BRISTOL N2
                                                        "Genome sequence of the nematode C. el investigating biology. The C. elegans Science 282:2012-2018(1998).
                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAR-1996) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197 GTSCE 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 --MVWDSHDKLGCAVVDCS-----GKTHVVCQYGPEAKGDGKTIYEEGAPCSRCSDYGA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 VHNTLRSRIAKGTYVAKGTAKPAASDMLKMKWDATVAASAQAYANKCPTGHSGAAGLGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 LHNGYRAAFARNYKTSK------MRTMVYDCTLEEKAYKSAEKCSEE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LYWYWTSATITNIDOFGA-----TGSAAWEKEFODYG--WSSNTLSMSLFNTGIGHA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----PSSEEENVDVFSAATLNIPLEAGNSWWSEIFELRGKVYNKNGKTSNIAN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVTCD 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOMAWAKTNLIGCGVKNCGKDINGFNKVTVVCQYKPQGNYLNQNIYTSGTTCSKCP---S 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21928 MW; 3DAFBCB60C6CC0E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.78;
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21,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26;
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Last
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Pred. No. 7.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence up
annotation
                                                                            elegans: a platform for ns Sequencing Consortium.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63; Indels
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                                  RESULT 34
093746
AC 09374
AC 09374
AC 09374
DT 01-FE
DT 01-FE
DT 01-FE
DT 01-FE
CO Chabco
OC Rhabco
OC Rhabco
OX NCBL
RN [1]
RP SEQUI
RN [2]
RP SEQUI
RN 110Ves
RI SCARR
RI INVes
RI SCARR
INVES
RI SCARR
RI INVES
RI INVES
RI INVES
RI INVES
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RI FERNIX
RI PRINX
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Query Match
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Submission.";
Submission.";
Submission.";
Submission.";
Submission.";
EMBL/GenBank/DDBJ databases
EMBL, AC024805, AAK39335.1;
InterPro. IPR001283; Allrgn_V5/Tpxl.
Pfam; PR00188; SCP; 1.
PRINTS; PR00037; V5TPXLIKE.
PRINTS; PR00037; V5TPXLIKE.
PRINTS; PR00037; STPXLIKE.
PRODOM; PD000542; Allrgn_V5/Tpxl; 1.
SMART; SM00198; SCP; 1.
Hypothetical protein.
SEQUENCE 246 AA; 26913 MW; B1D7D559DC07B399 CRC64;
                                                        InterPro; IPRO01283; Allrgn_V5/Tpx1
Pfam; PF00188; SCP; 1.
PRINTS; PR00837; V5TPXIIKE.
ProDom; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
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                                       SEQUENCE
                                                                                                                                                     investigating biology ";
Science 282:2012-2018(1998).
EMBL; Z70308; CAA94350 l; -.
                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
Eukaryota; Metazoa; Nemata
Eukaryota; Metazoa; Nemata
Rhabditidae; Peloderinae;
RCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                   Baynes C.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                        Genome sequence of the nematode C.elegans: A
                                                                                                                                                                                                                                                                                                                                                                 EQUENCE FROM N.A.
aynes C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               198 TTCD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 IIMTWYSQVNVGCGVKLCQKEGDYQLAIVVCKYWGEGQGNGKIMYESGPTCSACP---PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 --MVWDSHDKLGCAVVDCSGK----THVVCQYGPEAKGDGKTIYEEGAPCSRCSDYGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 ELHNGYRAAFARNYKTSK------MRTMVYDCTLEEKAYKSAEKCSEEPSSEEENVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 ------VFSAATLNIPLEAGNSWWSEIFELRGKVYNKNGKTSNIAN------- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 DAHNEFRSSIAKGTYVTKGLLHAPATNIMKMKWNVTIATAAQNHANKCPKGHDGPLEGVS 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .6 protein.
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45; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GECMWSGHINASKGVNHLGAVAAKAWSSE------YTKKGWETDVMSDEFFNSGVGHA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 02,
(TrEMBLrel. 02,
(TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                       8
                                                             Allrgn_V5/Tpx1; 1.
CP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Nematoda; Chromadorea; Rhabditida; Rhabditoidea; rinae; Caenorhabditis.
                                       22006 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.4%; Score 143.5;
24.5%; Pred. No. 1.7
Live 24; Mismatches
  14.38;
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cosmid Y51H7C.";
EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
Score 143;
                                       3072C43F25FFE626 CRC64;
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DB 5;
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Length
  207;
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P 69 P 69

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Best Local
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Best Local S
Matches 48
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Science 282.2012-2018(1989).
EMEL; 270307; CAA94332.1; -.
HSSP; P04288; 1CFE.
InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam; PF00188; SCF; 1.
PRINTS; PR00937; V5TPXLIKE.
PRODEM; PD000542; Allrgn_V5/Tpx1; 1.
SWART; SW00198; SCF; 1.
SWART; SW00198; SCF; 1.
SEQUENCE 210 AA; 23030 MW; 06AEA89;
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Q18540;
Q1-NOV-1996 (TIEMBLIEL 01,
Q1-JAN-1998 (TIEMBLIEL 05,
Q1-JUN-2002 (TIEMBLIEL 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
Eukaryota; Metazoa; Nemat.
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
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MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome sequence of the nematode C.elegans: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ubmitted (MAR-1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 YEEGAPCSRCSDYGAGVTCD 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 REMFTELHNGYRAAFARNYKTSK------MRTMVYDCTLEEKAYKSAEKCSEEPSSE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23
             194
                                                                   158
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46; Conservative 24;
                                                                                                                        134
                                                                                                                                                                                 106
                                                                                                                                                                                                                                83
                                                                                                                                                                                                                                                                                  69
                                                                                                                                                                                                                                                                                                                                           23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOGSGYGENLYWYWTSGTIGNLDTFGPA-----ASSSWESE------FQQYGWTSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QQAIVDAHNKLRSSIAKGTYVAKGTTQKSGSNMRKIKWDATVATSAQNYANTC---PTGH 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLDMNTFNTGIGHATQMAWANTFAIGCGVKNCGKDPSNGYNKVAVVCQYKTPGNYLNQPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EE-----NVDVFSAATLNIPLEAGNSWWSEIFELRGKVYNKNGKTSN 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YQQGTTCAACP---SGTACD
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 24.9
                                                                                                                                                                                                                                                                                      EENV------DVFS-----AATLNIPLEAGNSWWSEIFELRGKVYNK-----N
                                                                                                                                                                                                                                                                                                                                           KQSILNAHNDIRSRIAKGNYVAKGNRKESATNMLKMKWDSSLEQSAQNYANGCHMQHSTN 82
                                                                                                                                                                                                                                                                                                                                                                                REMETELHNGYRAAFAR-NY------KTSKMRTMVYDCTLEEKAYKSAEKCSEEPSSE 68
                SACP---AGTSCE 203
                                                                                                                     TGVAHATQIAWAPTGKIGCGVKNCGRDARRGGLFQVAIVCQYRVRGNFFFKNIYNSGATC
                                                                                                                                                                          GKTSNIANMVWDSHDKLGCAVVDCSG-----KTHVVCQYGPEAKGDGKTIYEEGAPC
                                                                                                                                                                                                                                DKTIGENLYWEWSGDPFSDLDKFGKIATVA-----WDHEFEQFGWNSNKFSLALFN
                                                                      SRCSDYGAGVTCD 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
:inae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23030 MW; 06AEA89CD24D0E2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.2%; Score 142; DB 5; Length 210; 24.9%; Pred. No. 1.9e-05; Live 23; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence up
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4; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   on update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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RESULT 36
08WS91
ID Q8WS9
AC Q8WS9
DT 01-WA
DT 11-WA
DT 1
      RESULT OF STREET OF STREET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ul-MAR-2002 (TERMBLrel. 20, Created)
01-MAR-2002 (TERMBLrel. 20, Last sequence update)
01-UN-2002 (TERMBLrel. 21, Last annotation update)
Putative esophageal gland cell secretory protein 13
HSP13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8WS91
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Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Heteroderidae; Heteroderinae; Heterodera.
NCBI_TaxID=51029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT 2000 (TremBLrel. 15, 01-OCT 2000 (TremBLrel. 15, 01-JUN-2002 (TremBLrel. 21, H10D18.2 protein.
SEQUENCE FROM N.A.

STRAIN-BRISTOL N2;

Madsen C., Tin-Wollam A., Keppler D.;

"The sequence of C. elegans cosmid H10D18.";

Submitted (MAR-1999) to the EMBL/GenBank/DDBJ

[3]
                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                           Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                     Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 HVVCQYGPEAKGDGKTIYEEGAPCSRCSDYGAGVTCD 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EAGNSWWSEI--FELRGKV-----YNKNGKTSNIANMVWDSHDKLGCAVVDC---SGKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WVVCNYKEAGNFLNOPVYKKGAACSKCSDYN-GATCD 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QACDMWWAELKQFGFQSSLVLDMAQFNKG--IGHWSQQAWASTAQIGCAMARCPSSTWKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.1%;
ilarity 33.0%;
Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed-11730789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 141; DB 5; Length 117; Pred. No. 1.2e-05; B; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  695F9502CE125D88 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117
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                                                  databases
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venom allergen-like
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133 72

SORRERE

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RESULT 38
018347
1D 01.834
AC 01.834
AC 01.834
DT 01.JA
DT 01.JA
DT 01.JA
DT 01.JA
DT 01.JA
OS D11rof
CC ELKRI
OC Oncho
ON NCBI.
RN [1]
RP FINE
RP FILE
RT SLEAT
DR FERMI
DR FERMI
DR Pfemm
DR SEQUE
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Best Local S
Matches 57
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Best Local Similarity 24.0
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1998 (TIEMBLIEL 05, Created)
01-JAN-1998 (TIEMBLIEL 05, Last sequence update)
01-JUN-2002 (TIEMBLIEL 21, Last annotation update)
Yenom allergen antigen 5-11ke protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro: IPR001283; Allrgn_V5/Tpxl.
pfam; PF00188; SCP; 1.
prinvs; Pr00837; V5TpxLIKE.
prinvs; Pr000842; Allrgn_V5/Tpxl; 1.
SMART; SM0128; SCP; 1.
SEQUENCE 208 AA; 22470 MM; 917E0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Waterston R.;
Waterston R.;
Submitted (WAR-2000) to the EMBL/GenBank/DDBJ databases
Submitted (WAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AC006655; AAB39874.1;
                                                                                                                                                                                                                                                                                                                                                                                           sera.";
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF001100; AAB52535.1;
InterPro; IDR001283; Allrgn_Y5/Tpxl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dirofilaria immitis (Canine heartworm).

Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Dirofilaria.

MCBI_TaxID-6287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *SEQUENCE FROM N.A.

*Dirofilaria immitis larval cDNA clone isolated with immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            018347
                                                                                                                                                                                                                                                                                                    PRINTS; PR00837; V5TPXLIKE.

ProDom; PD000542; Allrgn_V5/Tpx1; 1.

SMART; SM00198; SCP; 1.

PROSITE; PS01010; SCP_AG5_PR1_SC7_2; UNKNOWN_1.

SEQUENCE 221 AA; 25158 MW; 5542B42B455046F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 KLGCAYVDCSG-----KTHVVCQYGPEAKGDGKTIYEEGAPCSRCSDYGAGVTCDD 171
                                                   100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 HNDLRSAIALGNYDAAGTIEPPAANMRKIKWDSTVASSAQQYANTCPDDHSGTEYGENLY 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 HNGYRAAFA-RNY-----KTSKMRTMYYDCTLEEKAYKSAEKCSEEPSSEEENVDVF
                                                                                                                                                         19
                                                                                  78
                                                                                                                     57
                                                                                                                                                                                            7
                                                                                                                                                                                                                                  Similarity 27.0
                                                                                                                                                                                              CQQREKLDDDMREMFTELHNGYRAAFARNY------KTSKMRTMVYDCTLEEKAYK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KIGCGVKNCGKDSSMNNMYKVAVVCQYDQAGNMMDSDIYQSGDTCSFCP---SGSKCEE 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WSWSSSAPTSLDKFGVAASNSWEKEFQDYGWESTY-MDADLFDSG--IGHATQMAWAETN 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAATLNIP-----LEAGNSW------WSEIFELRGKVYNKNGKTSNIANMVWDSHD 120
                                                                                                                 SAEKC--SEEPSSEE----ENVDVF-------SAATLNIPLEAGNSWWSEIFELRG
                                                                                                                                                         CEGGKLTPTERKNIVTQI-NKYRSRLIRGKLKNKDGYLMPKGKNMLRHRWDCKLEKSAQN 77
                                                   KVYN---KNGKTSNIA------NMVWDSHDKLGCAVVDCSGKTH------VVCQ 138
                                                                                      WANMCVFGHSPSSERRGIGENVYAYWSSGSVRDLKKTAGT-----DAGRLWWSEL----E
               KYYSDNPSNNLTSEVAMENILHFTQMAWGETYKLG-----SGVDHNIVMVARTLVFICH 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22470 MW; 917E04AD6C1DBF33 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.1%; Score 141; DB 5; Length 208; 24.0%; Pred. No. 2.4e-05; Indels 38; tive 28; Mismatches 70; Indels 38;
                                                                                                                                                                                                                                14.1%; Score 141; DB: 27.0%; Pred. No. 2.5e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            221 AA
                                                                                                                                                                                                                                                    DB 5;
2.5e-05;
                                                                                                                                                                                                                                  65; Indels
                                                                                                                                                                                                                                                                   Length 221;
                                                                                                                                                                                                                                72;
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                                                                                      128
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40
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Best Local Similarity
Matches 47; Conserv
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q18549 PRELIMINARY;
Q18549; Q20610;
01-NOV-1996 (TIEMBLIEL 01,
01-NOV-1998 (TIEMBLIEL 08,
01-UN-2002 (TIEMBLIEL 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copper J., Cooper J.,
Craston M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Craston M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Johnston L.,
Johnston L.,
Johnston L.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen F.
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
Cleans T., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0837; V5TPXLIKE.

PRODOM; PD000542; Allrgn_V5/Tpxl; 1.

SMART; SM0198; SCP_AG5_PR1_SC7_2;

PROSITE; PS01010; SCP_AG5_PR1_SC7_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Sims M.;
Submitted (MAR-1996)
                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE-94150718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wature 368:32-38(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ubmitted (MAR-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183
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                                                     132
                                                                                        111 IAN------MVWDSHDKLGCAVVDCS-----GKTHVVCQYGPEAKGDGKTIYEEG
155 APCSRCSDYGAGVTCD 170
                                                                                                                            82
                                                                                                                                                               66
                                                                                                                                                                                              22 ESTQQFIVDLHNKLRTSIAKGTYVAKGTTKAAGSNLLKMKWDTTLATAAQTFANTCPRGH
                                                                                                                                                                                                                                  15 DDMREMFTELHNGYRAAFARNYKTSKMRT-----MVYDCTLEEKAYKSAEKCSEEP
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                                                     LANTGIGHATQMAMANTGLIGCGYKNCGPDPELNNYNRAVVVCQYKAQGNYLGQDIYKSG
                                                                                                                            SNAAGVGENLYWRWSSLPFSGMDIYGG------AASVAWEQEFQQYG--WTTNTFTQA 131
                                                                                                                                                             SSEE---EN------VDVFSAATLNIPLEAGNSWWSEIFELRGKVYNKNGKTSN 110
                                                                                                                                                                                                                                                                                                                                               211 AA;
                                                                                                                                                                                                                                                                   14.1%; Score 140.5; DB 5; Length 2 ilarity 24.0%; Pred. No. 2.7e-05; Conservative 25; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                      SCP; 1;
0; SCP_AG5_PR1_SC7_2; UNKNOWN_1.
0; SCP_AG5_PR1_SC7_2; UNKNOWN_1.
AA; 22676 MW; ADF90C8E263F58F2 CRC64;
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Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Mshi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Staubli F., Suzuki R., Tomita M., Magner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sasaki J., Boffelli D., Bojunga N., Carninci P., Ge Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kandya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kandya M., Lee N.H.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Nasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Kohtsuki S.,
RA Hayashizaki Y.,
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Best Local
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Q9CQ35;
01-JUN-2001 (TremBLrel. 1
01-JUN-2001 (TremBLrel. 1
01-JUN-2002 (TremBLrel. 2
492150801111k protein.
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RATURE 409:685-690(2001).
EMBL; AK01884; BAB29994.1; -.
EMBL; AK01884; BAB29994.1; -.
HSSP, P04284; ICEE.
HSSP, P04284; ICEE.
MGD; MGI:1914787; 4921508011R1k.
InterPro; IPRO01283; Allrgn_V5/Tpx1.
Pfam; PF00188; SCP; 1.
Pfam; PF00188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
PRINTS; PR00837; V5TPXLIKE.
SMART; SMO0198; SCP; 1.
SMART; SMO0198; SCP; 1.
SMART; SMO0198; SCP; 1.
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STRAIN-C57BL/6J; TISSUE-TESTIS;
MEDLINE-21085660; PubMed-11217851;
Kawai J., Shinagawa A., Shibata K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hayashizaki Y.;
    41
                                                                                                             212
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                                                                                                                                                                                YGAGVTCDD 171
                                                                                                                                                                                                                                                   QLVWDSSYKVGCAVTSCARAGGFTHAALFICNYAP----GGTLTRRPYQAGQFCSRC-- 211
                                                                                                                                                                                                                                                                                                                                                                                              HESHPVFTEIGENMWVGPVEDFTVTTAIRSWHEE----RKSYSYLNDTCVEDQNCSHYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EENVDVFSAATLNI---PLE-----AGNSWWSEIFELRGKVYN------KNGKTSNIA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDDMREMETELHNGYR-AAFARNYKTSKMRTMVYDCTLEEKAYKSAEKCSEEPSSE----
                                                                                                        -GPGDQCTD
                                                                                                                                                                                                                                                                                                                      NMVWDSHDKLGCAVVDCS---GKTHV----VCQYGPEAKGDGKTI----YEEGAPCSRCSD 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DVDFINEYVGLHNELRGTVFPPGV---NLRFMTWDVALSRTARAWGKKCMYSRNTHLDKL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.1%; Score 140.5; DB.1; Length 332; Larity 29.1%; Pred. No. 4.7e-05; Conservative 20; Mismatches 67; Indels 47;
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                                                                                                        219
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RESULT 42
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ID Q2242
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RP SEQUENCE FROM N.A.

RC STRAIN-C57BL/GJ; TISSUD-PANCREAS;

RX MEDLINES-21085660; PubMed-11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Alzawa K., Izawa M., Nishi K., Riyosawa H., Kasukawa T., Saito R.,

RA Aizawa K., Izawa M., Nishi K., Riyosawa H., Kasukawa T., Saito R.,

RA Aizawa K., Jawa M., Nishi K., Riyosawa H., Kasukawa T., Saito R.,

RA Aizawa K., Jawa M., Nishi K., Riyosawa H., Kasukawa T., Saito R.,

RA Aizawa K., Jawa M., Carlon J., Bono H., Basukawa T., Satoka H.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,

RA Sato K., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyo-oka K., Wang K. H., Weitz C., Whittaker C., Wilming L.,

RA Hayashizaki Y.,
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Best Local S
Matches 48
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HSSP; P04284; ICFE.
MGD; MGI1926142; 1810049K24R1k.
InterPro; IPR001283; Allrgn_V5/Tpx1.
InterPro; IPR004043; LCCL_dom.
Pfam; pP00188; SCP; 1.
PRINTS; PR00837; V5TXLIKE.
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Q9D2R3;
Q1-JUN-2001
01-JUN-2001
Q22421
Q22421;
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Probom; PD000542; Allgn_V5/Tpxl; 1.

SMART; SM00198; SCP; AG5_PR1_SC7_2; 1.

PROSTTE; PS01010; SCP_AG5_PR1_SC7_2; 1.

SEQUENCE 434 AA; 48593 MW; C25067E814647AC0 CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 Similarity 25.8
48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     PLEAG-----NSWWSEIFEL-----RGKVYNKNGKTSNIANMVWDSHDKLG
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                                                                                                                                                                                                                                         CAVHTCRNMNVWGDTWENAVYLVCNYSPKGNWIGEAPYKHGRPCSECPSSYGGGCL----
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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                           PRELIMINARY;
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                              PRT;
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Query Match
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018539
01-NOV-1996 (TIEMBLIFEL 0
01-JAN-1998 (TIEMBLIFEL 0
01-JUN-2002 (TIEMBLIFEL 2
C39E9.5 protein.
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01-NOV-1996 (TrEMBLrel. (
01-JUN-2002 (TrEMBLrel. 2
T12A7.3 protein.
                                                                                                                                                                                                                  Caenorhabditis elegans.
Eukaryota: Metazoa: Nematoda: Chromadorea: Rhabditida; Rhabditoidea:
Rhabditidae: Peloderinae: Caenorhabditis.
NCBI_TaxID=6239;
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Probom; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
PROSTIE; PS00092; N6_MTASE; UNKNOWN_
SEQUENCE 262 AA; 29919 MW; 1B51A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 investigating blology.";
Science 282:2012-2018(1991).
EMBL; Z73911; CAS98140.1;
InterPro; IPR001283; Allrgn_V5/Tpx1.
InterPro; IPR002052; N6_Mtase.
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                    Submitted (MAR-1996)
"Genome sequence of the nematode C.elegans: investigating biology.";
                                                                  SEQUENCE FROM N.A.
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-1996)
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; 29919 MW; 1B51A10F5F603ABA CRC64;
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26.2%; Pred. No. 4
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Best Local S
Matches 46
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Science 282:2012-2018(1998).
EMBL; Z7037; CAA94330.1; -.
HSSP; P04284; ICFE: Allrgn_V5/Tpx1.
Interpro; ITR001283; Allrgn_V5/Tpx1.
Pfam; PF00188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
PRINTS; PR00837; V5TPXLIKE.
PRODOM; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
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SMART; SM00198; SCP; 1.
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Q18538;
Q1-NOV-1996
Q1-JAN-1998
Q1-JUN-2002
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Pfam; PF00188; SCP; 1.

PRINTS; PR000837; V5TPXLIKE.

Prodom; PD000542; Allrgn_V5/Tpx1; 1.

SMARF; SM0128; SCP; 1.

SEQUENCE 209 AA; 22319 MW; 50504
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Eukaryota; Metazoa; Nematoda;
Rhabditidae; Peloderinae; Caer
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EMBL; 270307; CAA94331.1; -.
HSSP; P04284; ICFE.
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MEDLINE-99069613; PubMed-9851916;
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                                                                                                                                 Similarity 24.3
46; Conservative
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Matches

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114 -MVWDSHDKLGCAVVDC------SGKTHVVCQYGPEAKGDGKTIYEEGAPCSRCSDYG
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                                                                            KSYGENLEWAYSSSPITDLDKYYQSAVDTWYSE-FQMFG--WNSNKFTTALWNTGIGHAT
                                                                                                        EENVDVFSAATLNIPL-----EAGNSWWSEIFELRGKVYNKNGKTSNIAN------
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QVAWSATGQVGCGAKNCGADSVRVGSYKATIVCQYKVPGNYLFKNIYNSGAKCSACP---
                                                                                                                                                                   KQSMVNAHNAVRSSIAKGEYVAKGTKKDSATNMLKMKWDNSLAQSAQNYANGCPMQHSPD
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Pred. No. 4e
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                                                                                                                                                                                                                                                       Mismatches
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SOR BERRY REAL STREET

209 ξ

Created)
Last sequence up update)

oda; Chromadorea; Rhabditida; Rhabditoldea; Caenorhabditis.

EMBL/GenBank/DDBJ databases

Genome sequence of the nematode C.elegans: A platform for

22459 MW; D9A915316027AFAA CRC64;

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1D 018539
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QQFIVDLHNSFRSKLATGTYSINGTLKPAGSNIRKMSWDSTLATSAQTYANTCPTGFSNT REMFTELHNGYRAAFARNYKT------SKMRTMYYDCTLEEKAYKSAEKCS-----21; Mismatches Score 137.5; DB Pred. No. 5e-05; DB 5; 75; Indels Length 209; 47; Gaps 84 107 62